

FIGURE 1

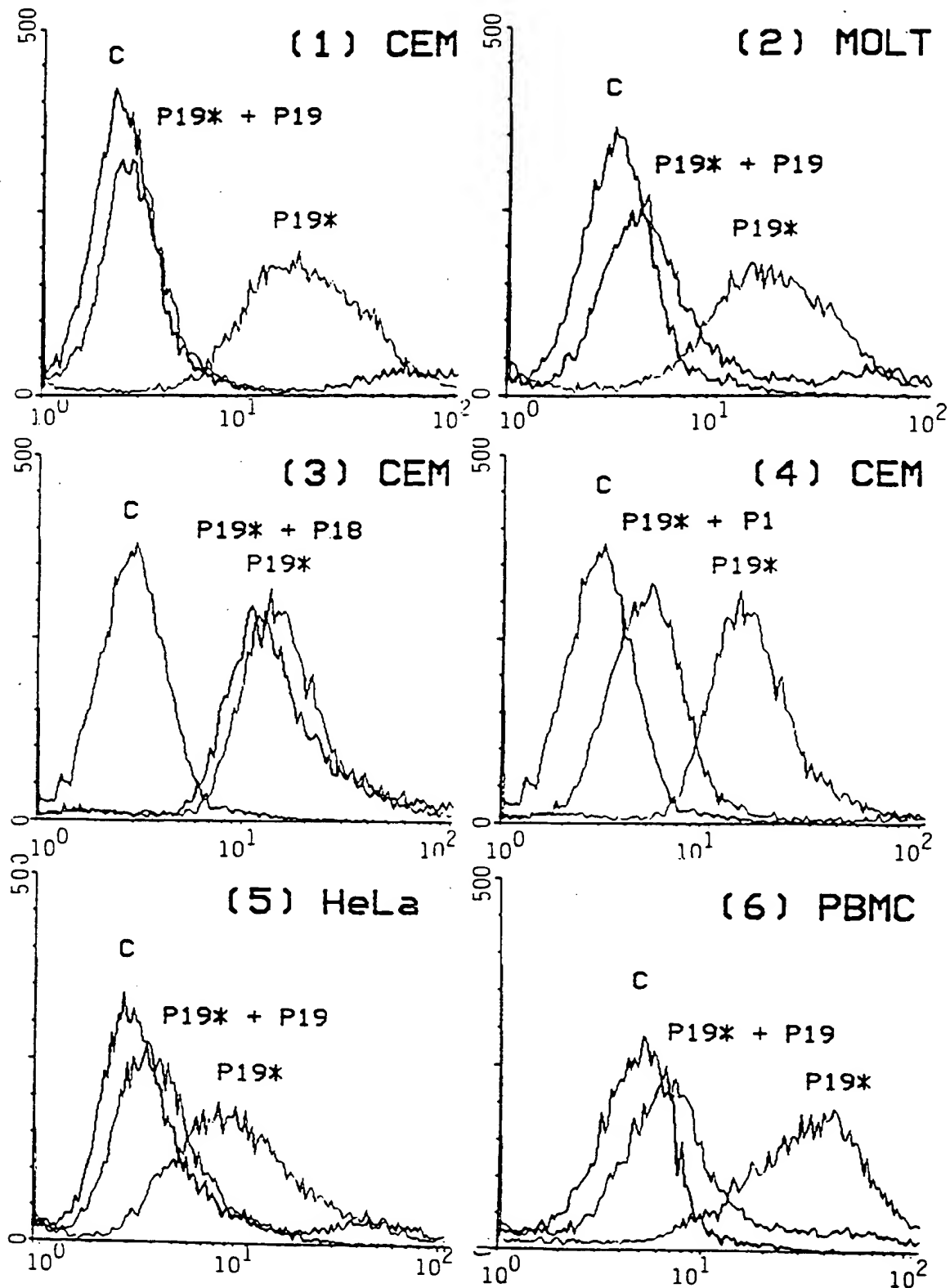


FIGURE 2

SELECTED PREFERENCES:

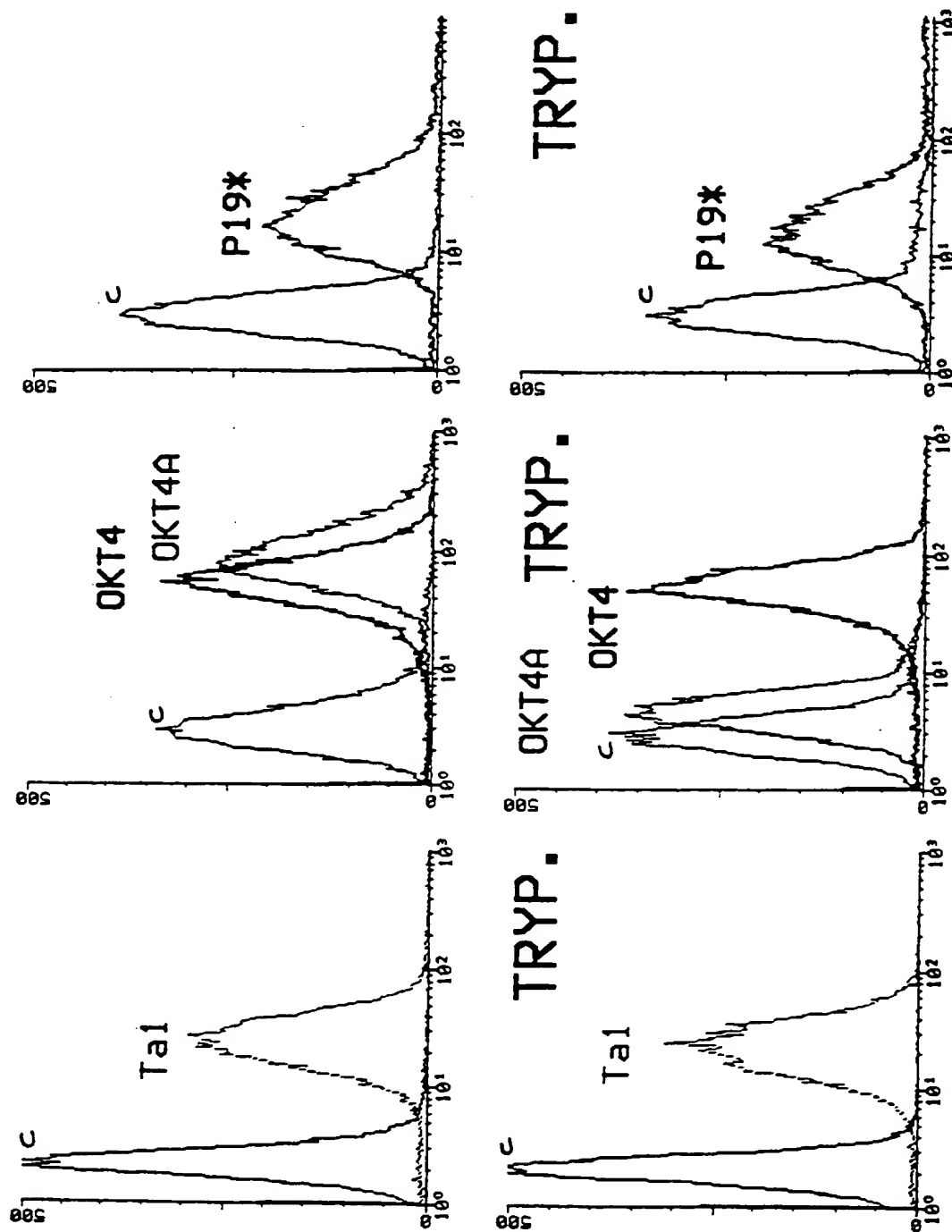


FIGURE 3A

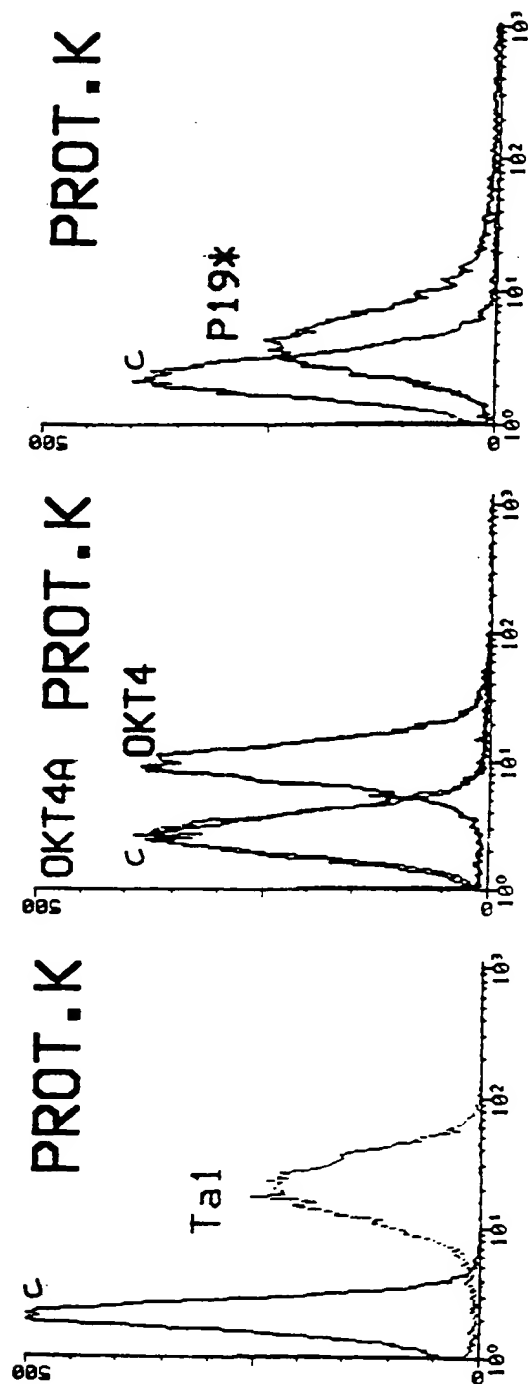


FIGURE 3B

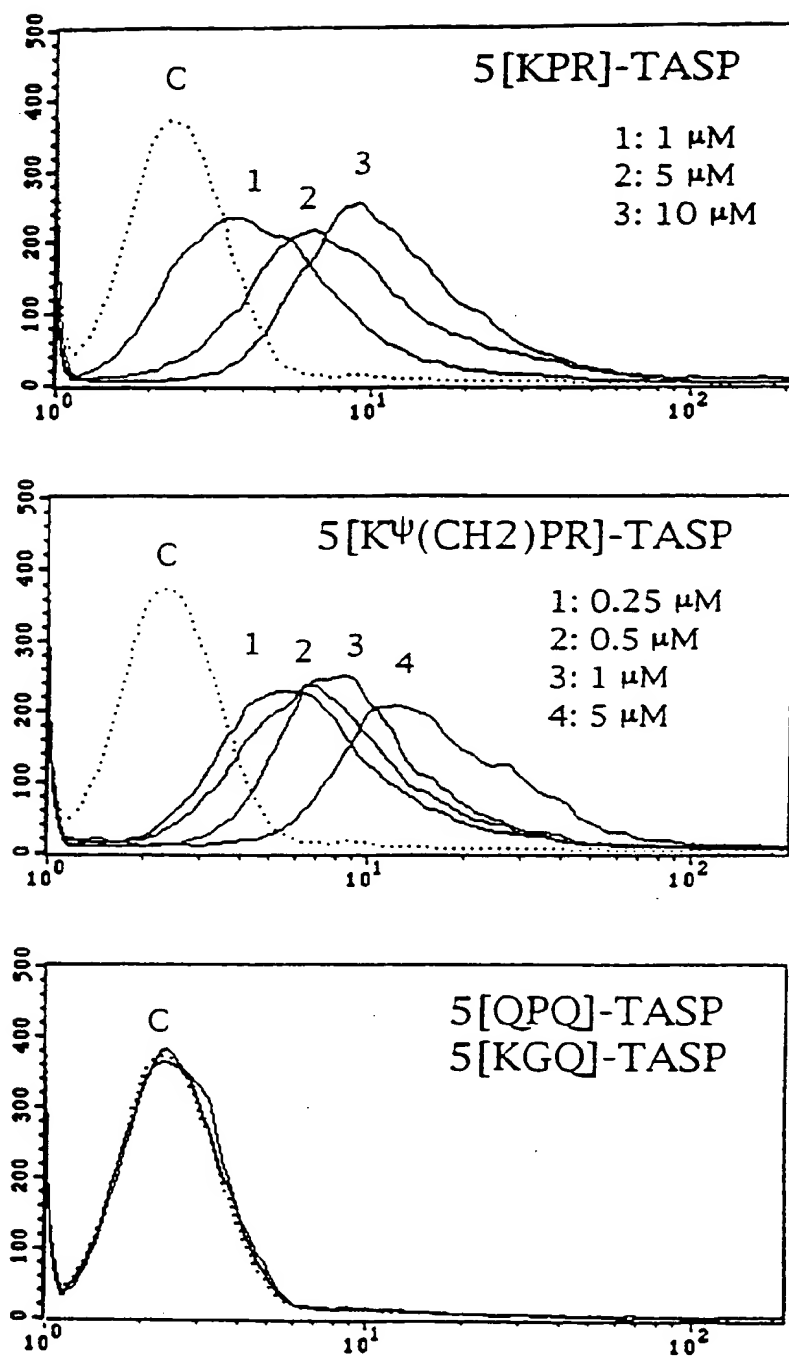


FIGURE 4

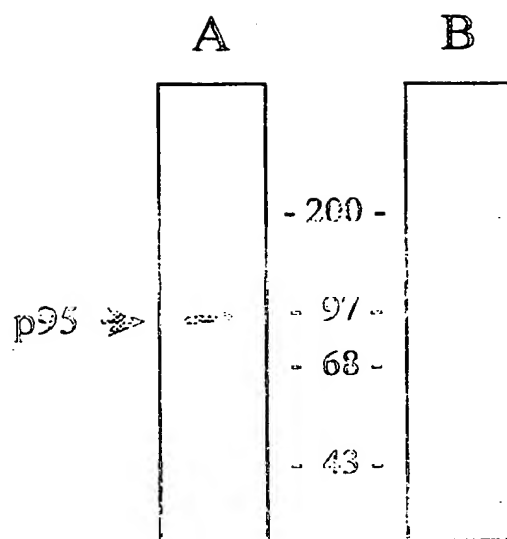


FIGURE 5

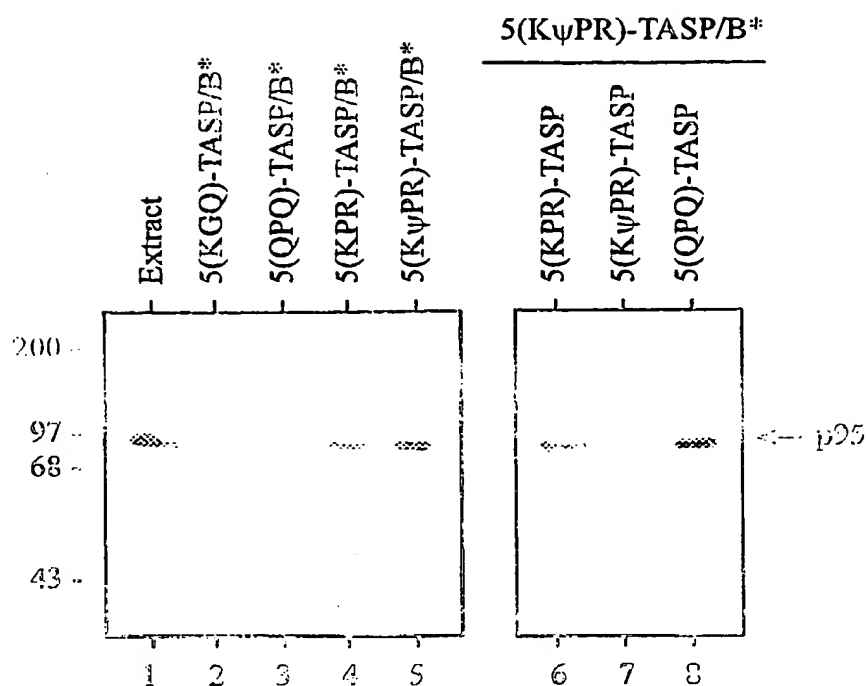


FIGURE 6

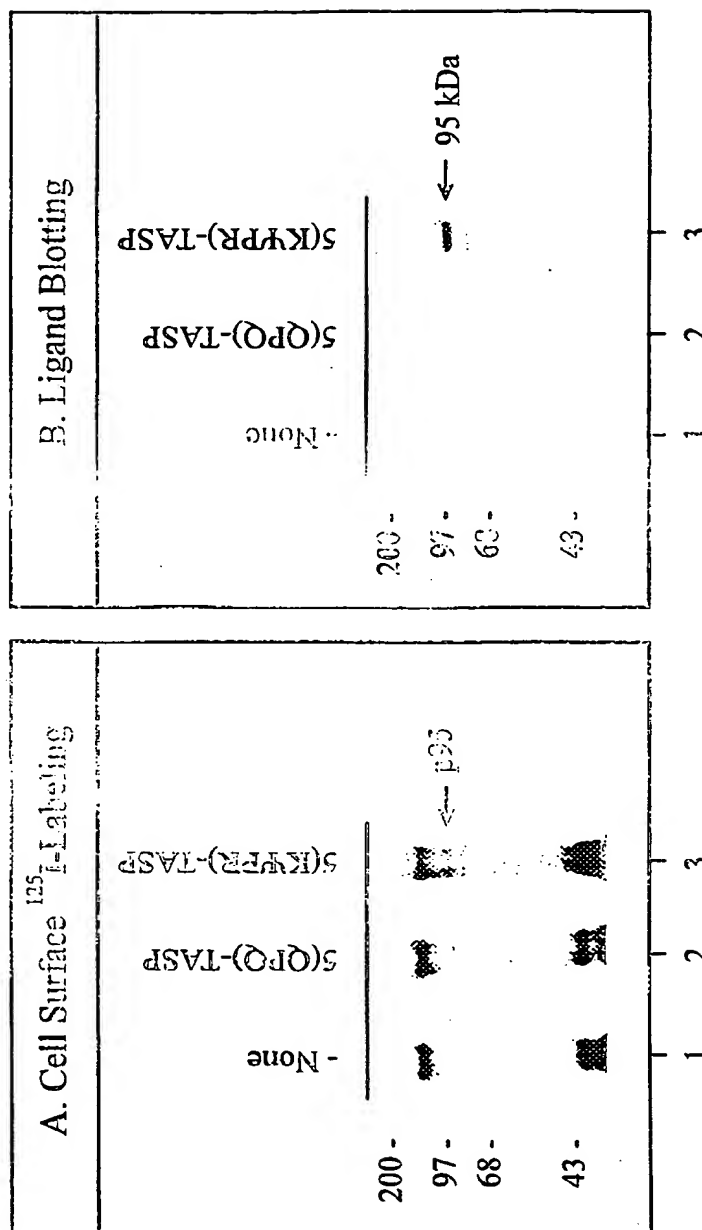


FIGURE 7



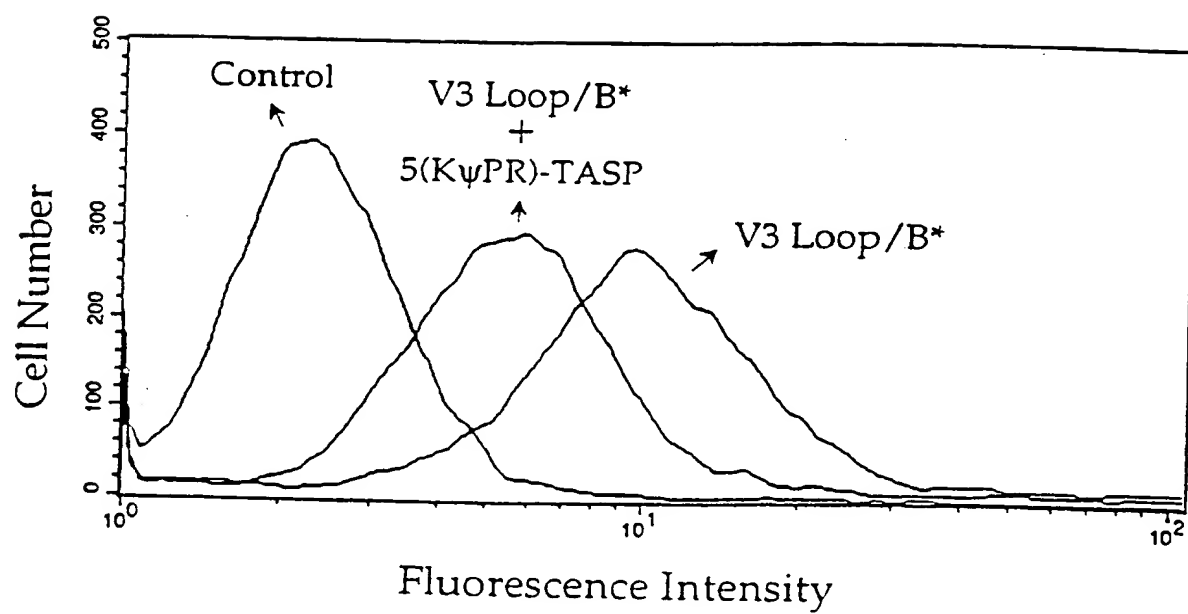


FIGURE 8A

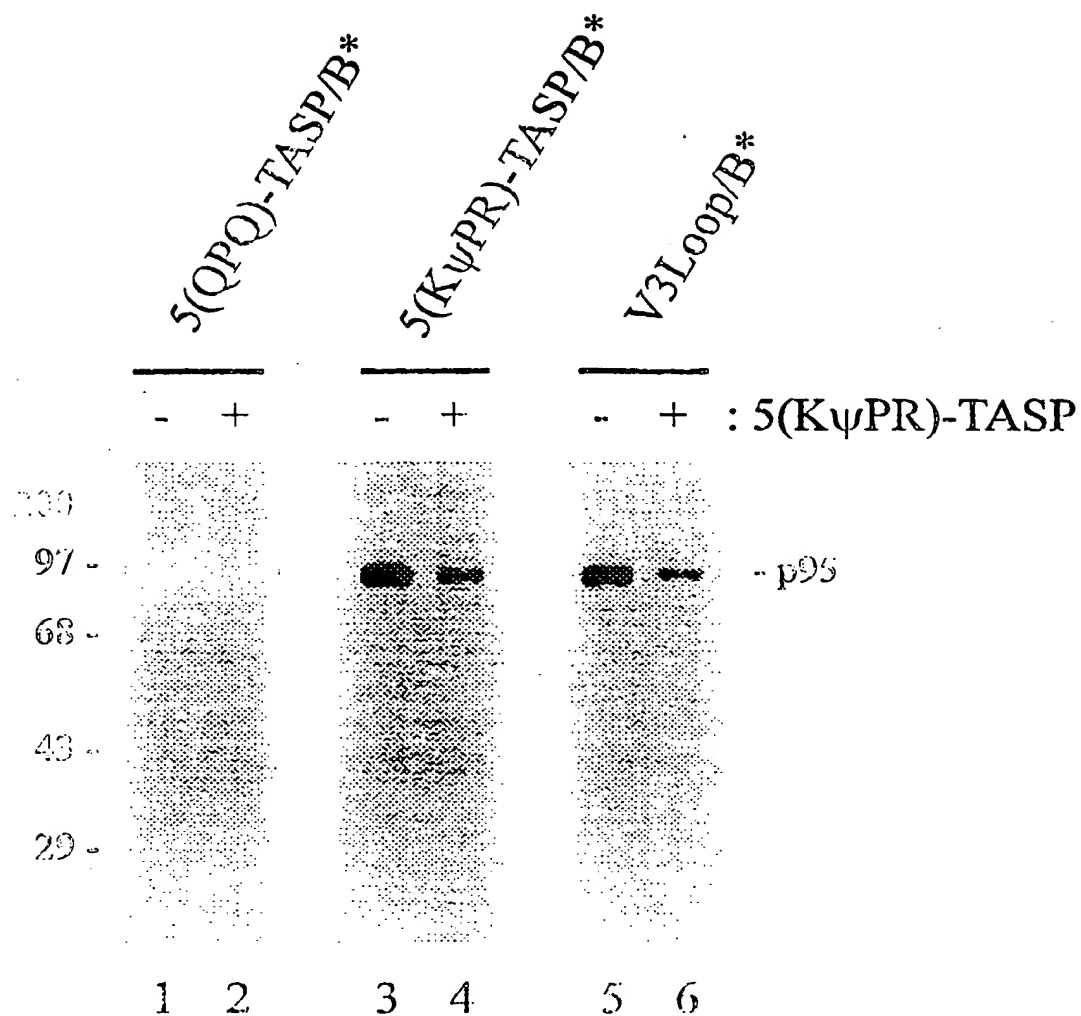


FIGURE 8B

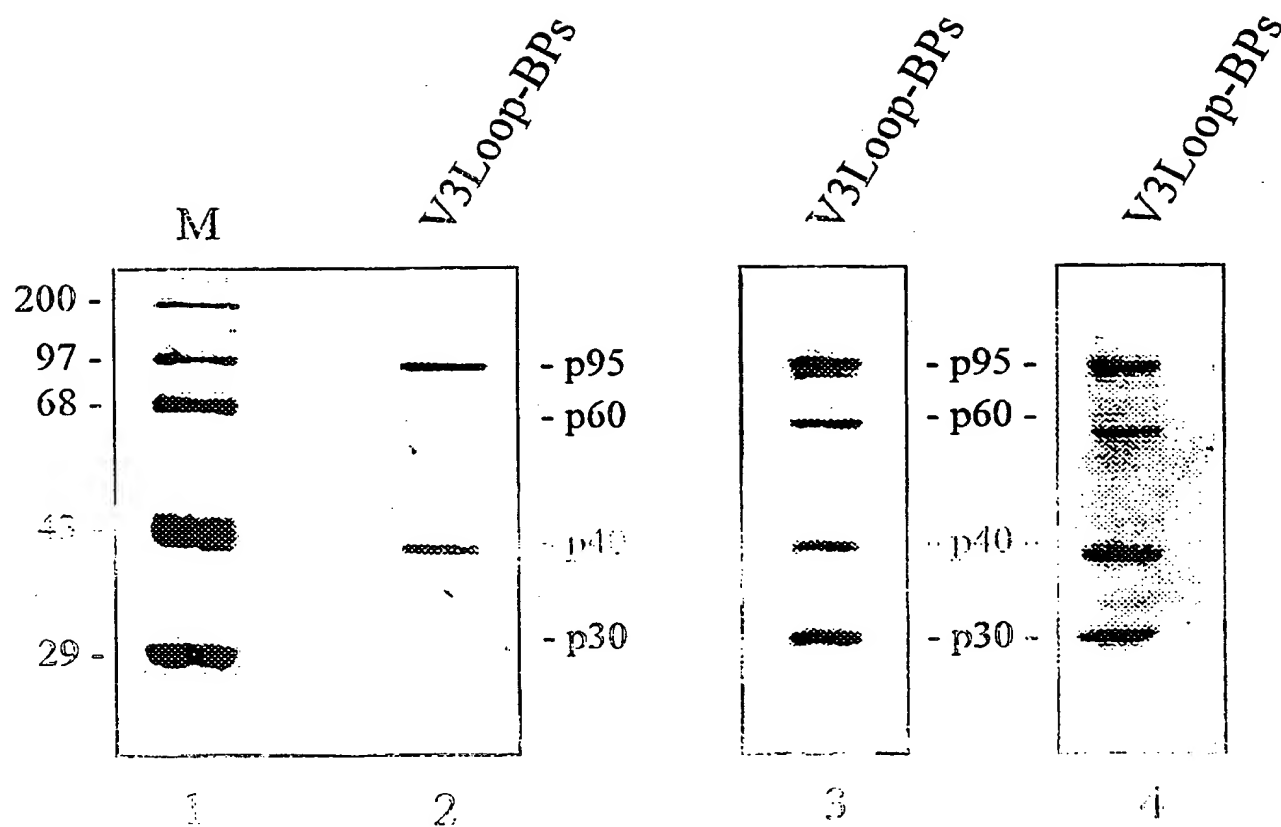


FIGURE 9

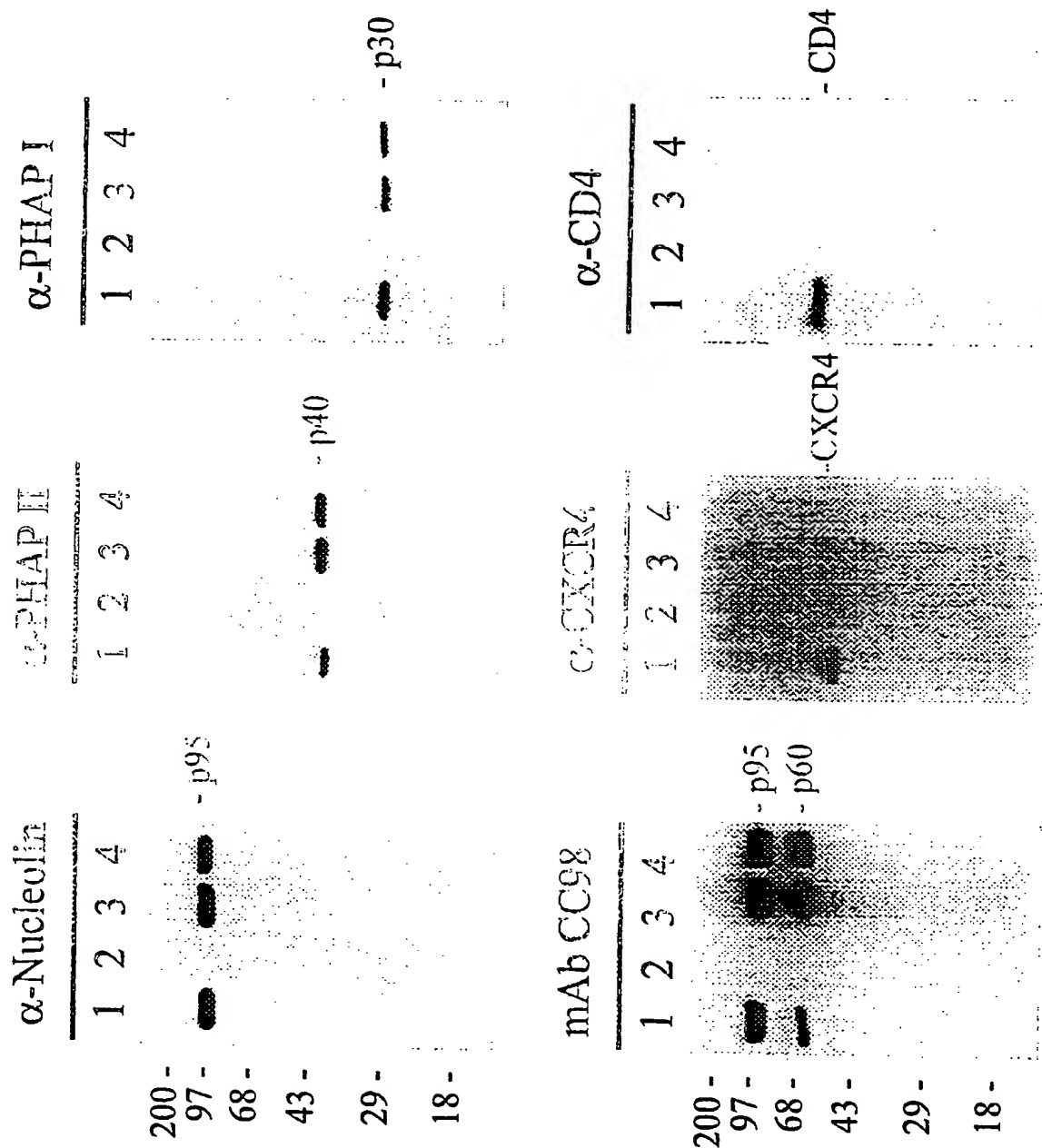


FIGURE 10

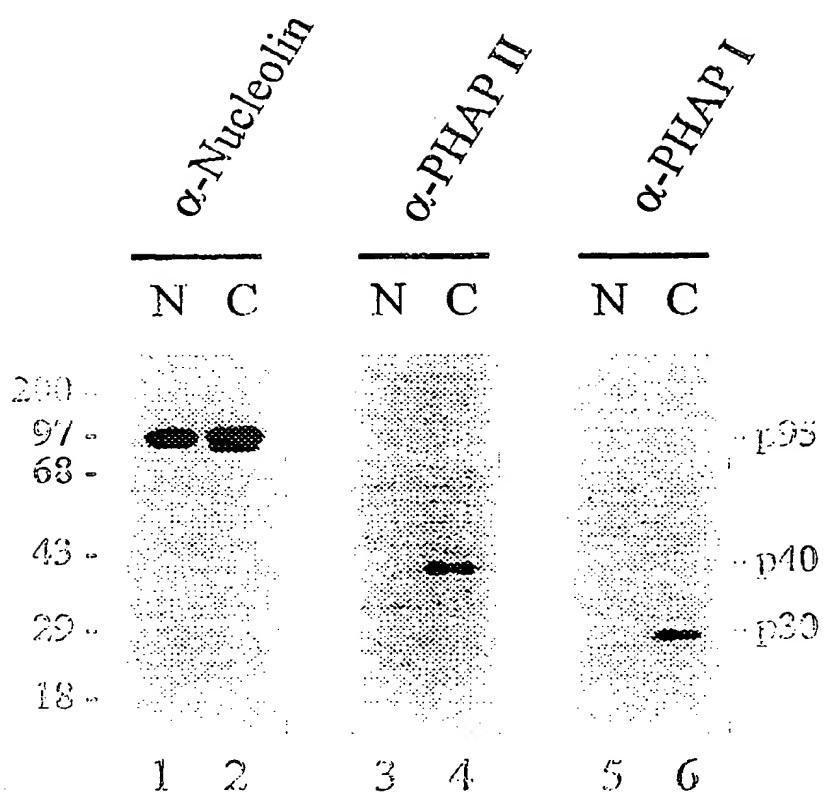


FIGURE 11

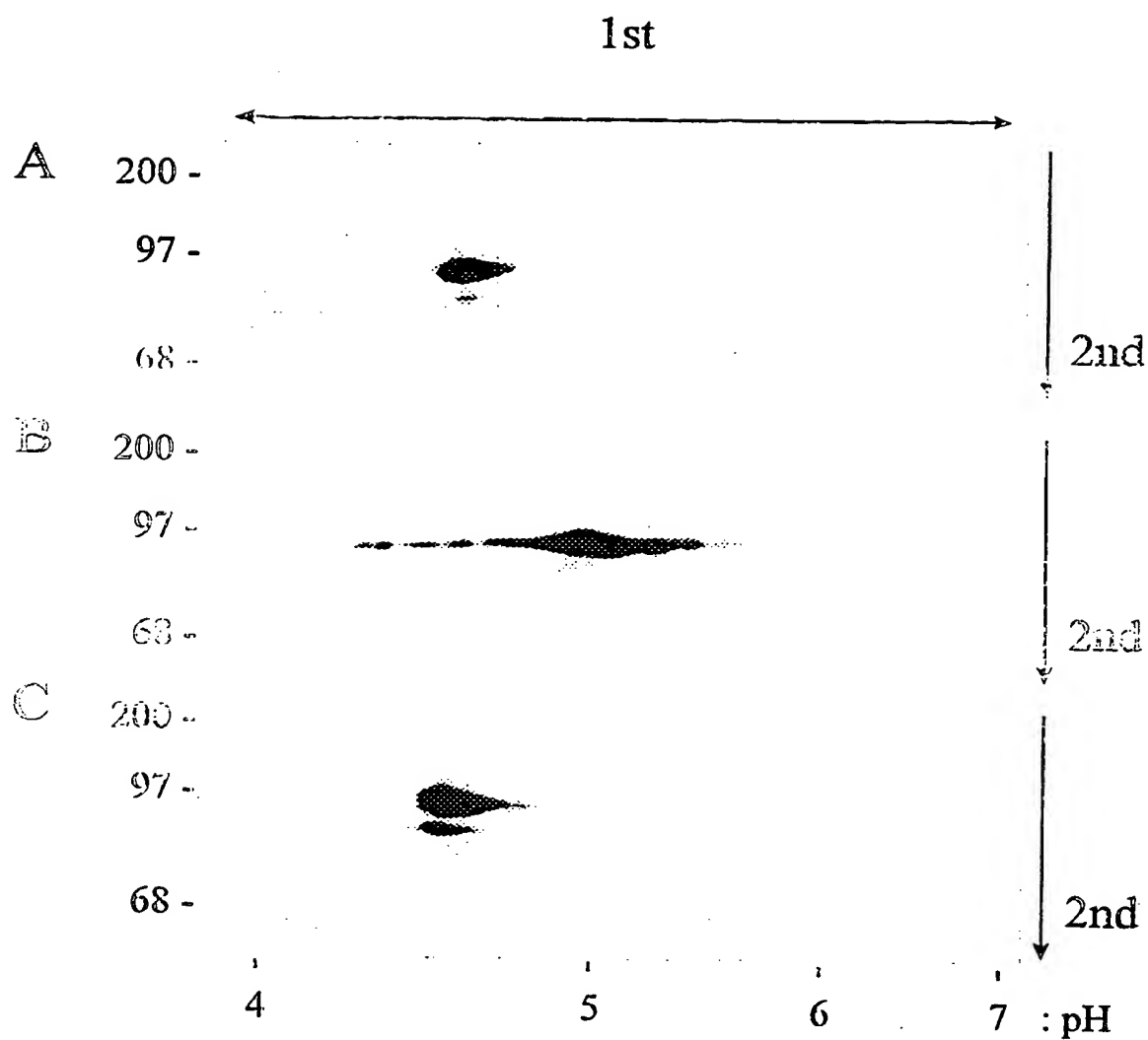


FIGURE 12

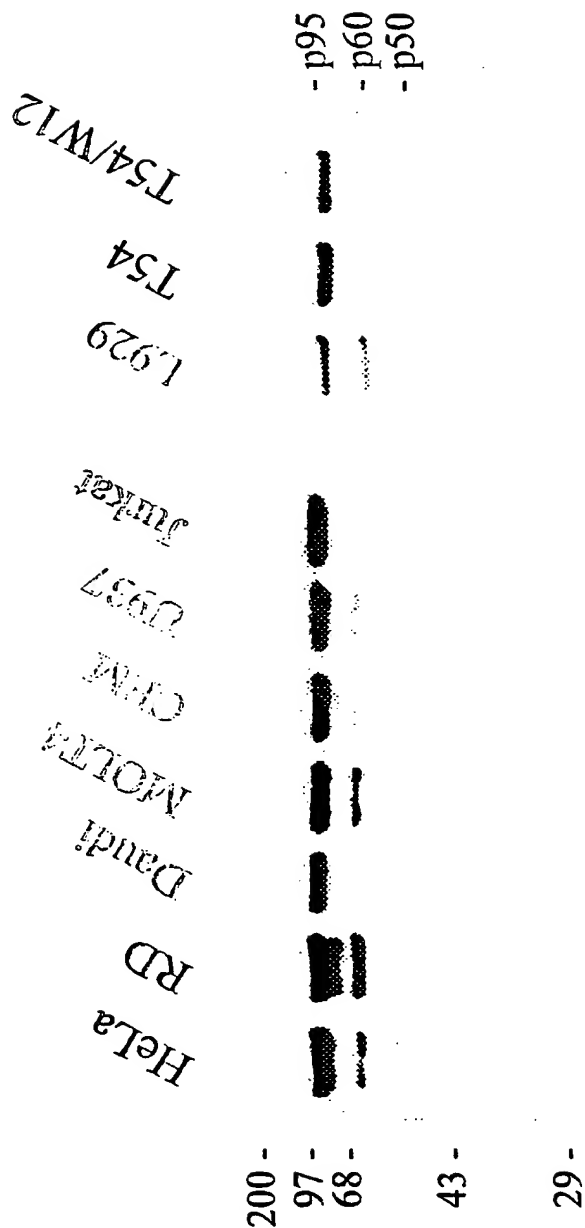


FIGURE 13A

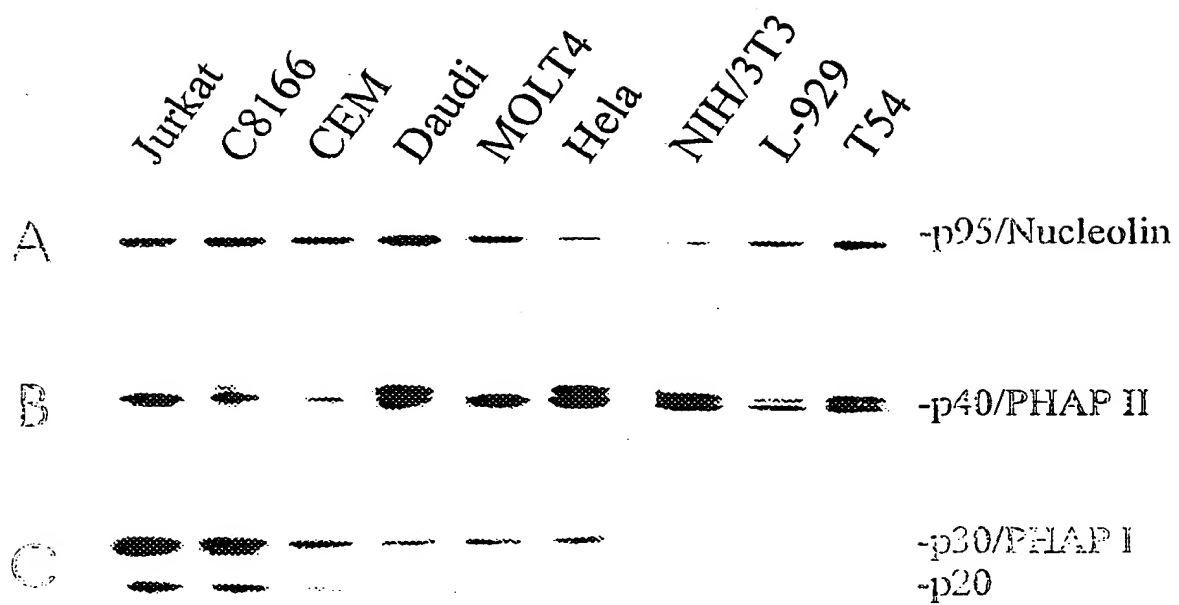
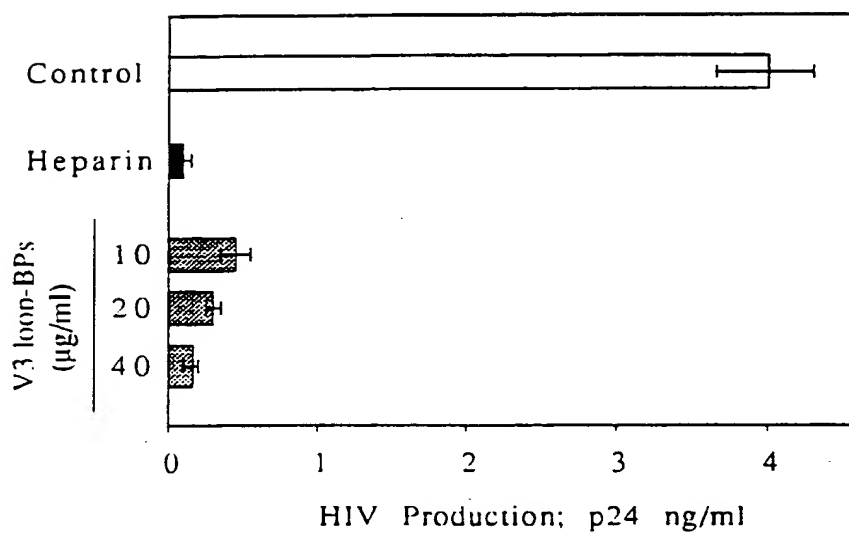


FIGURE 13B



A.



B.

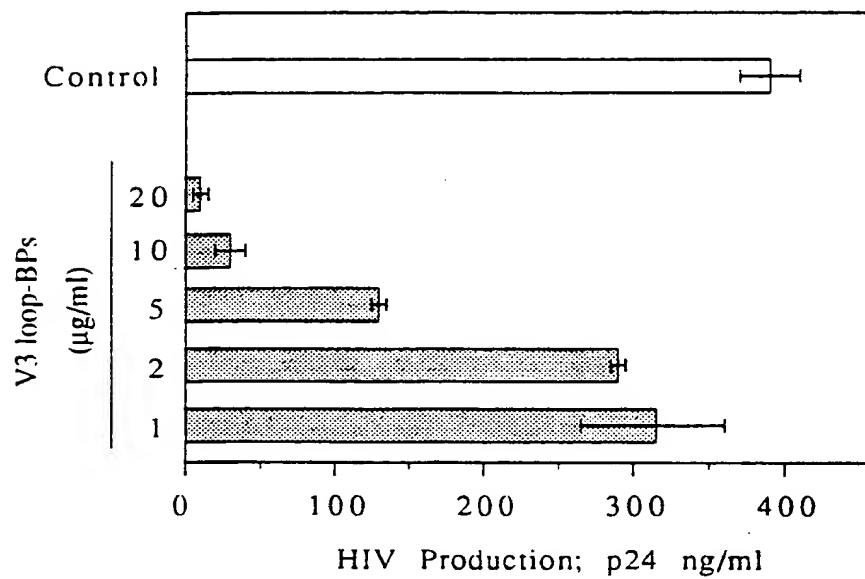


FIGURE 14

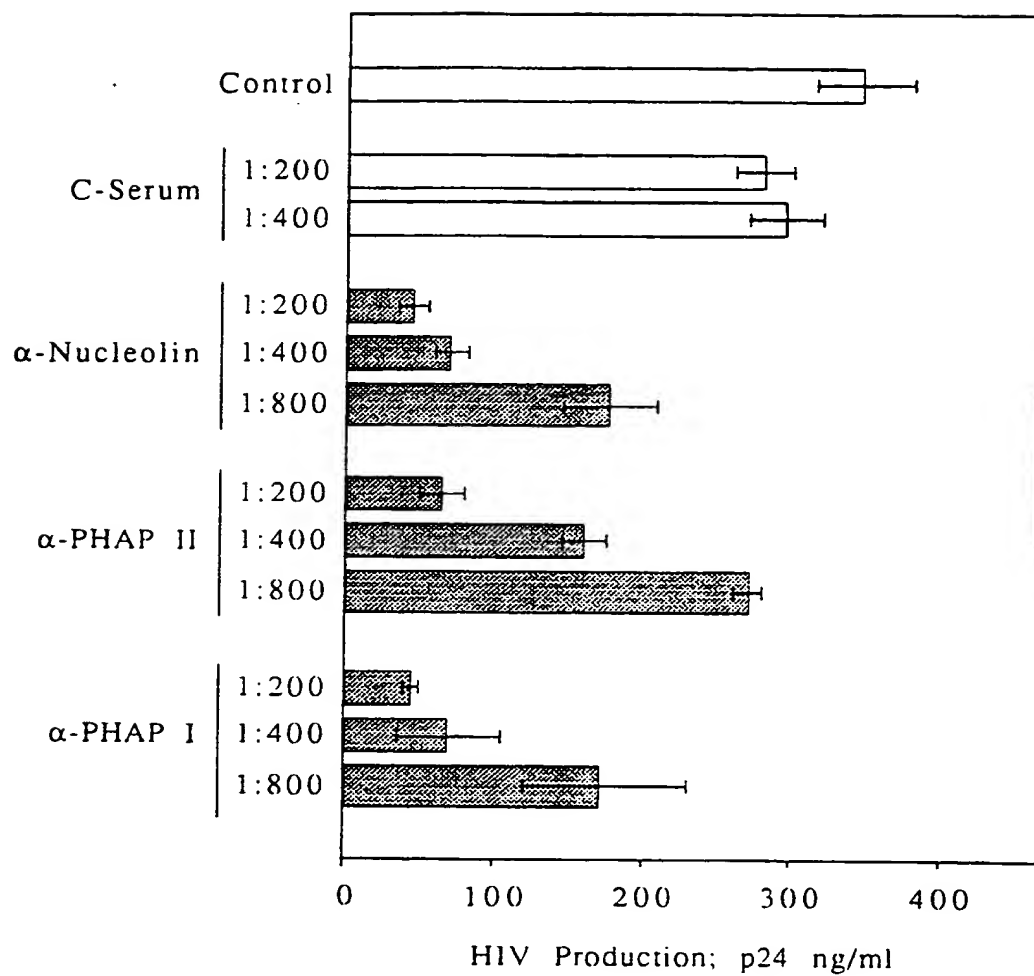


FIGURE 15

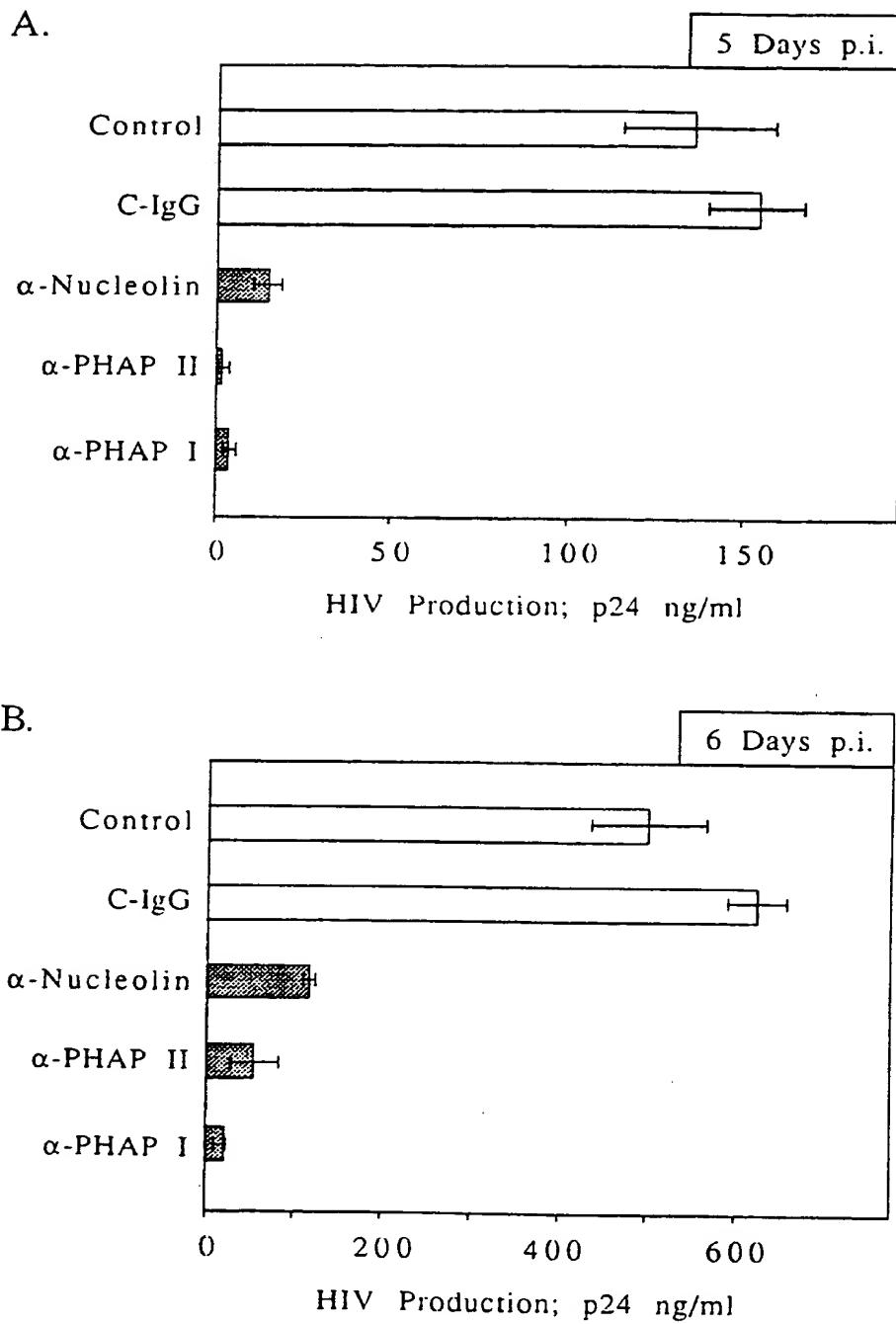


FIGURE 16

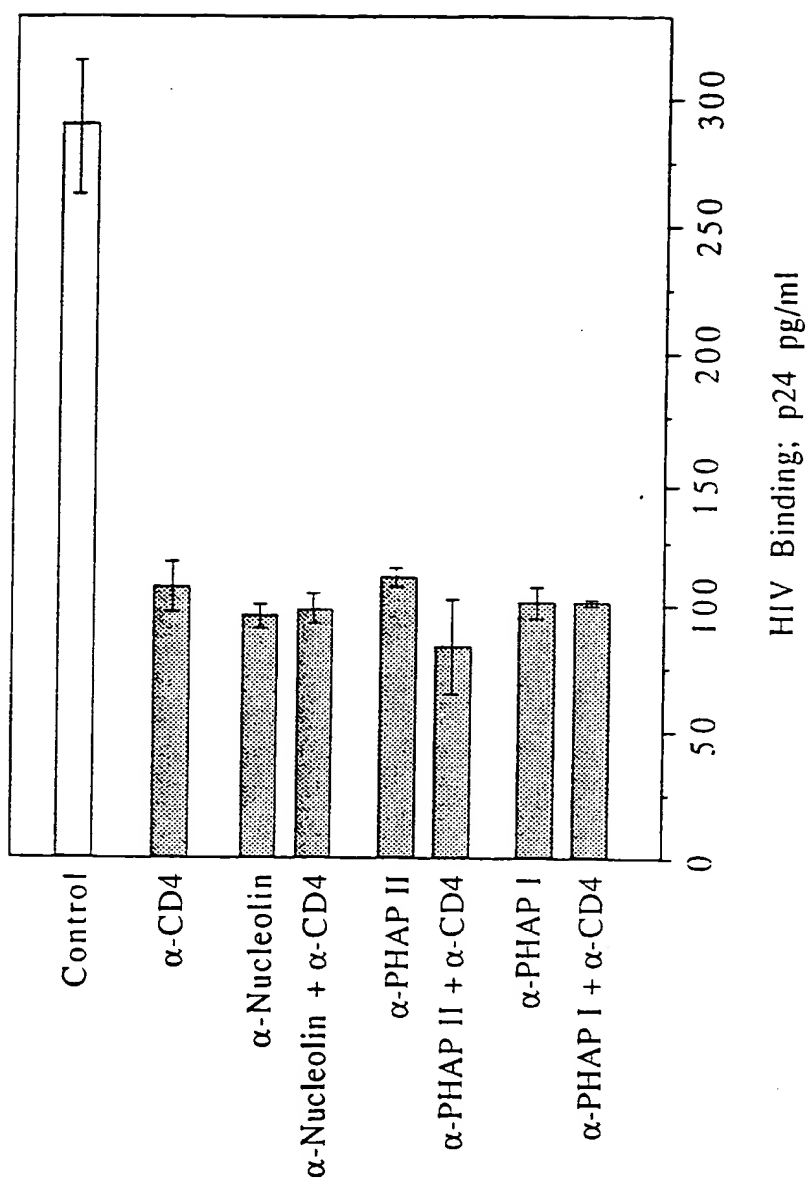


FIGURE 17

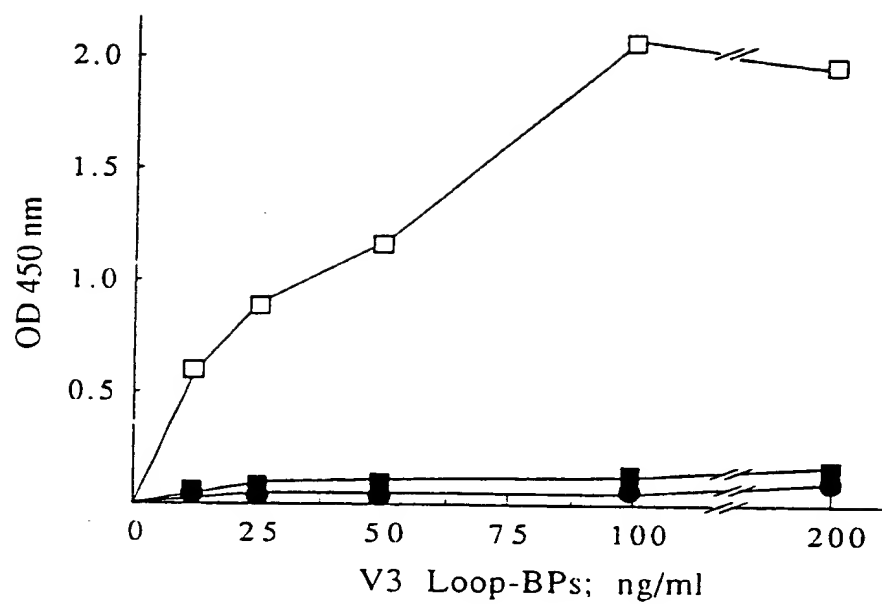


FIGURE 18

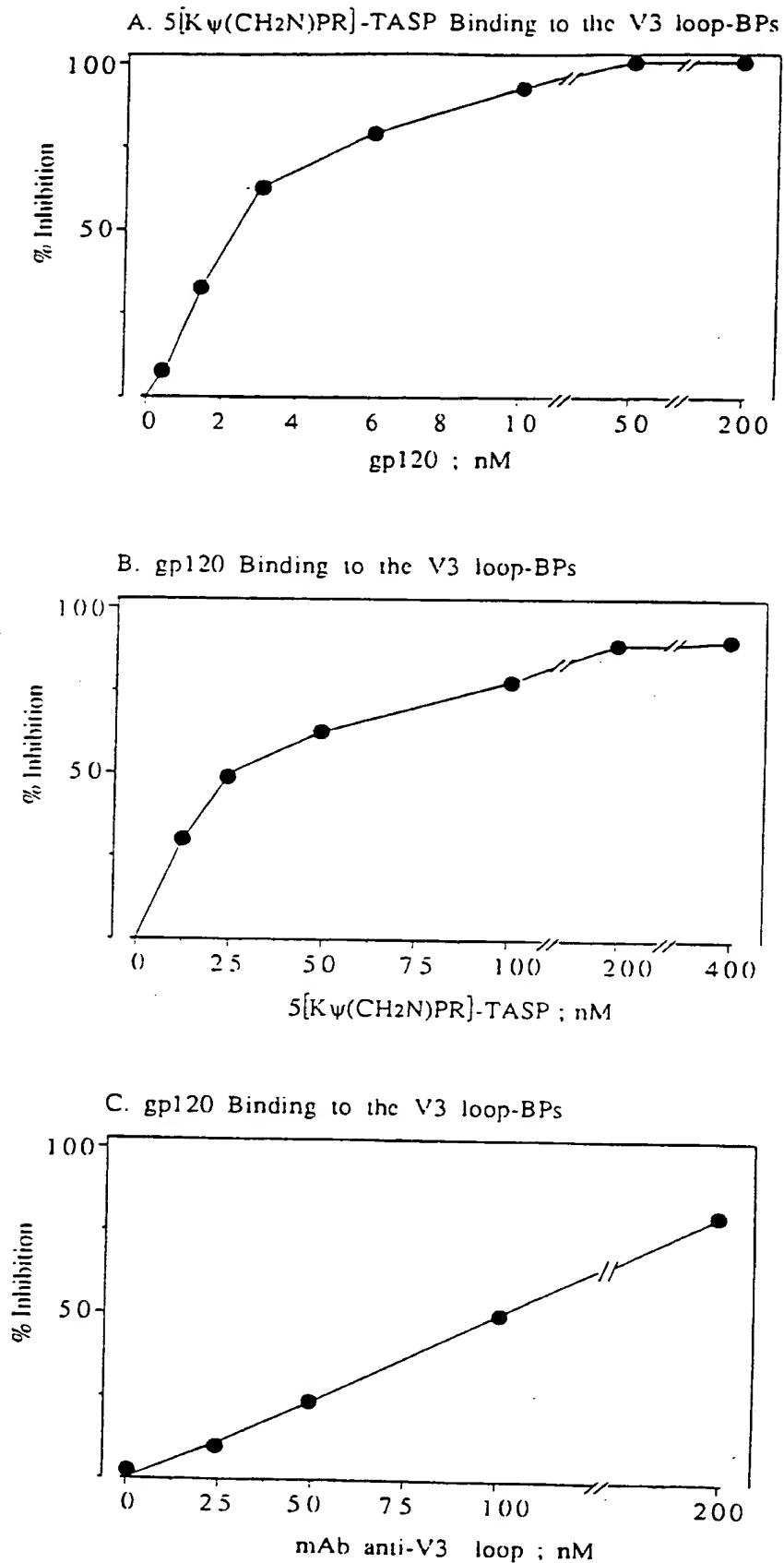


FIGURE 19

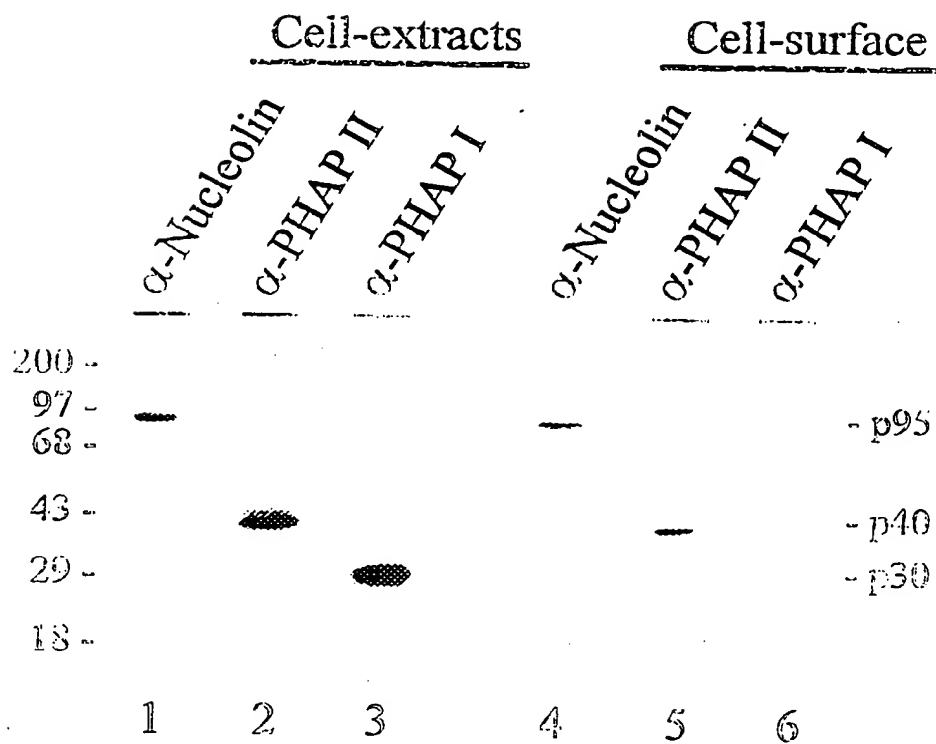


FIGURE 20

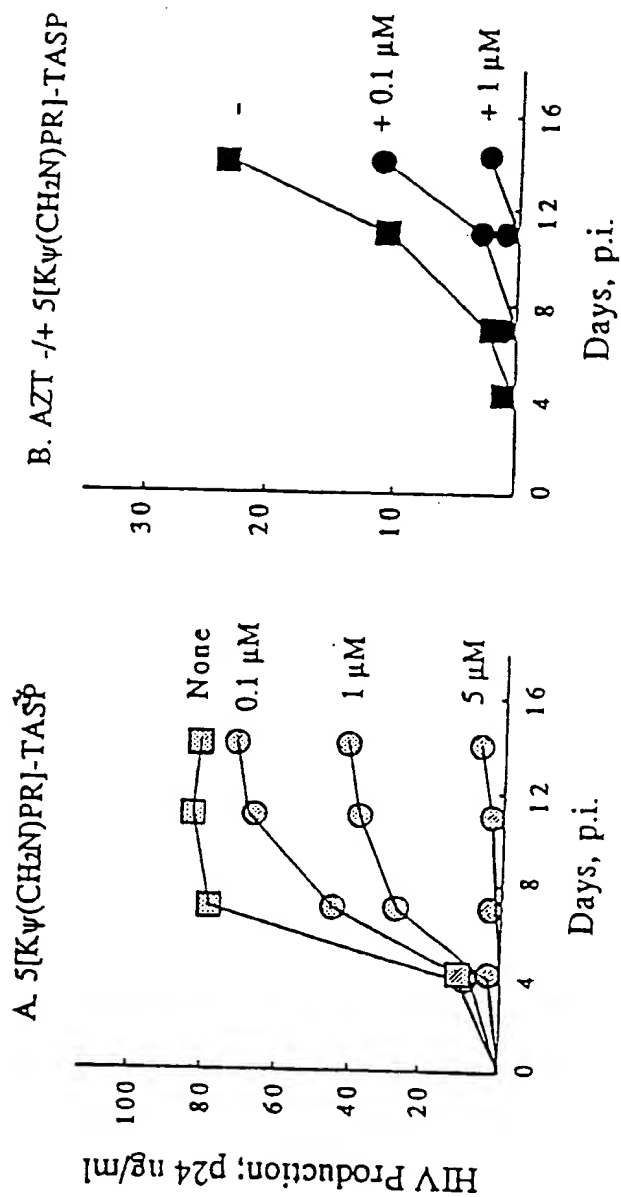


FIGURE 21



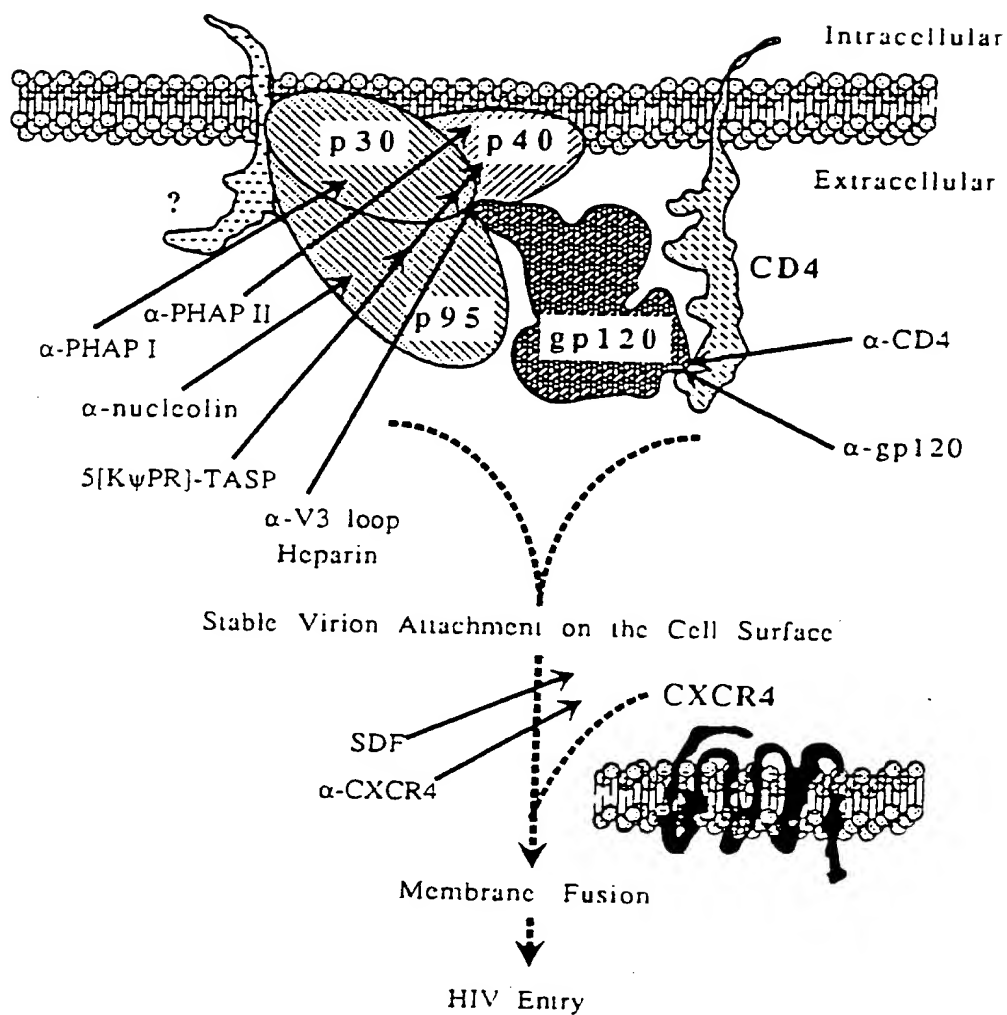


FIGURE 22

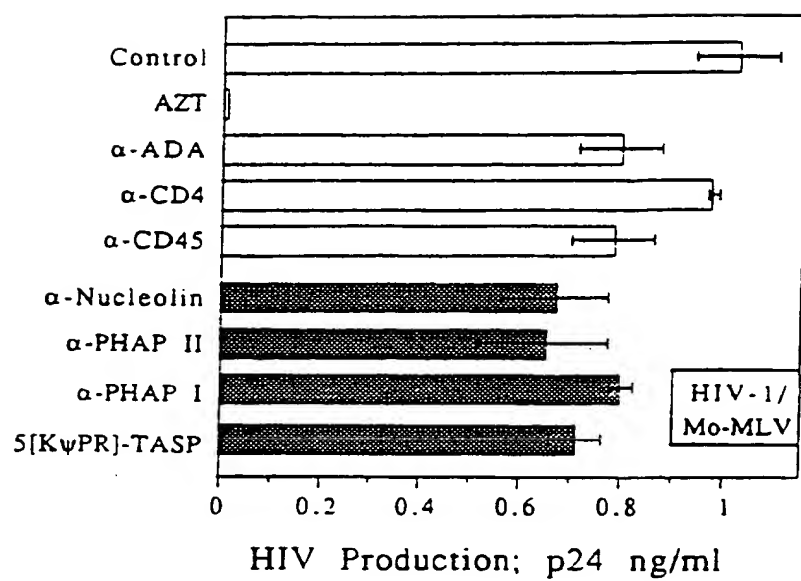


Figure 23

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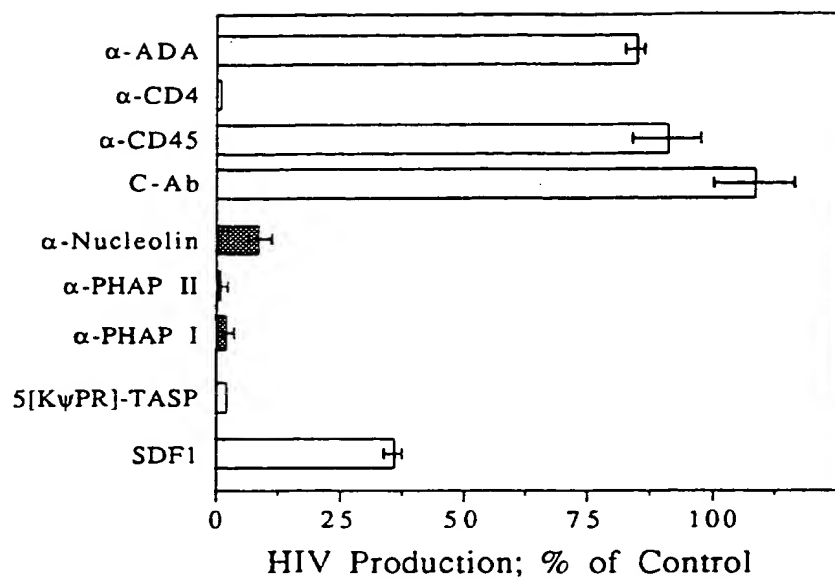


Figure 24

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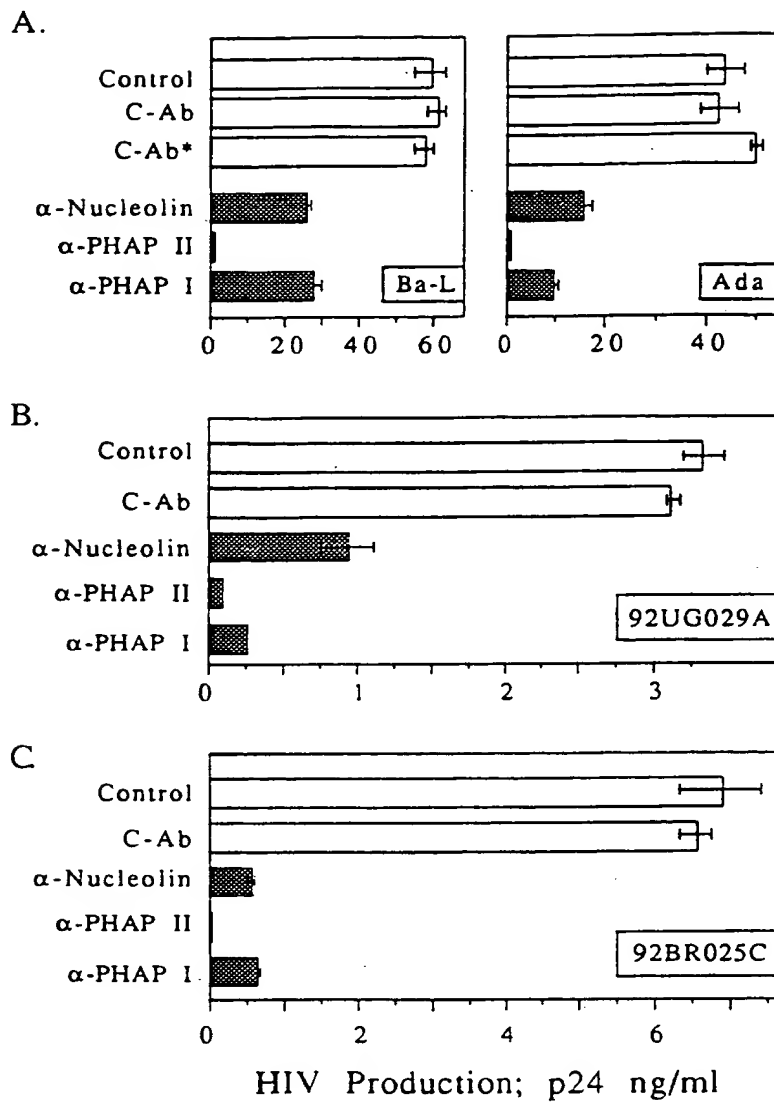


Figure 25

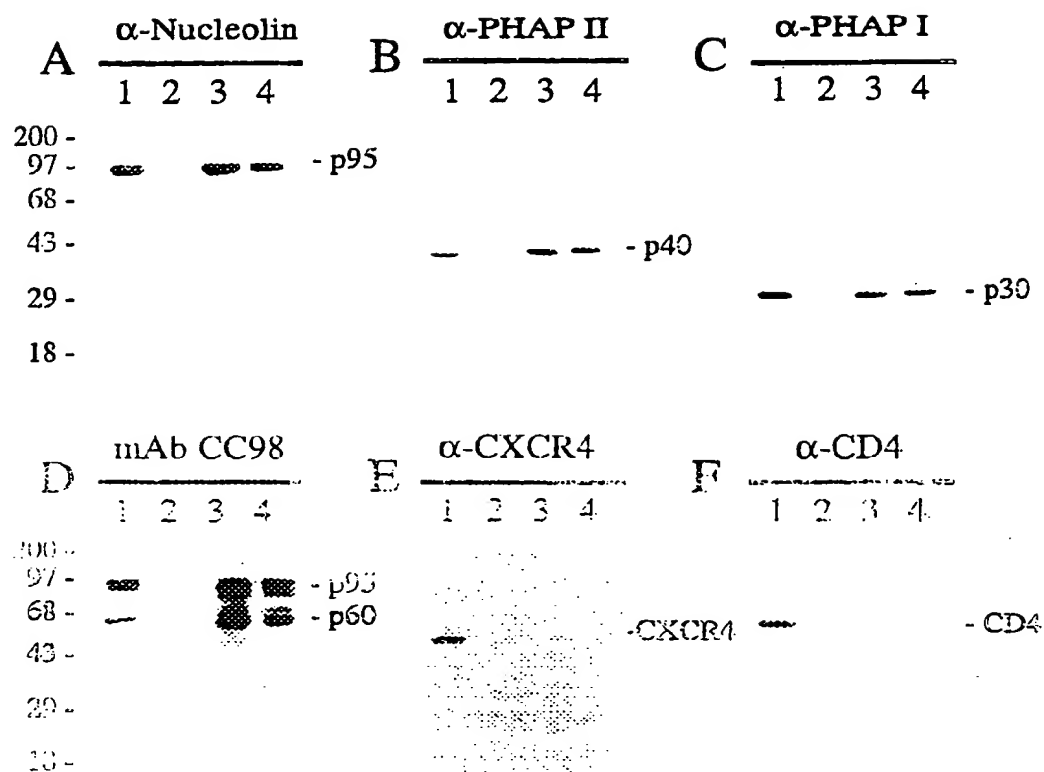


Figure 26

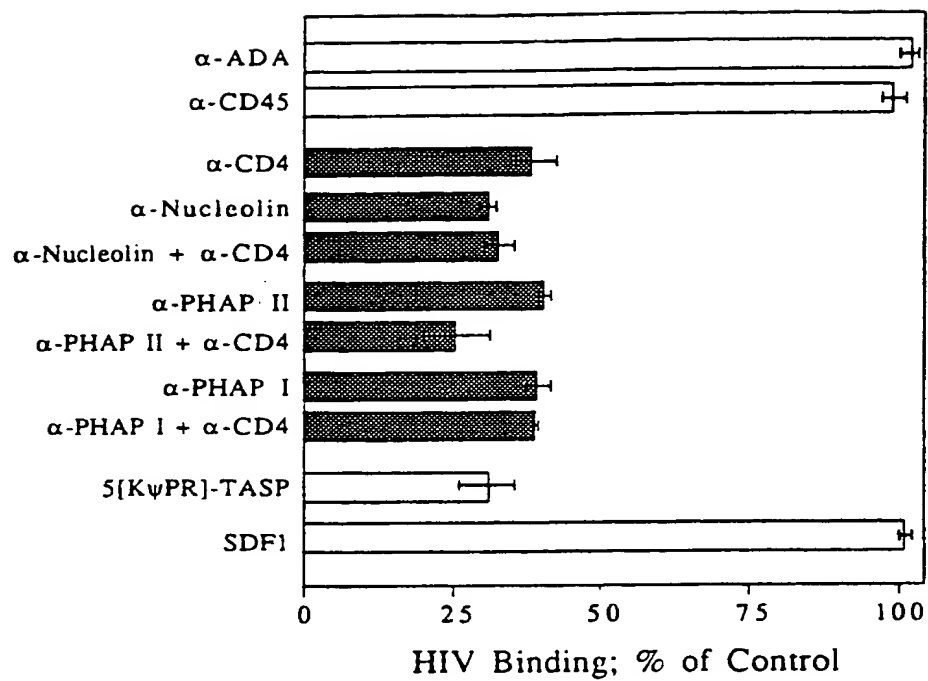


Figure 27

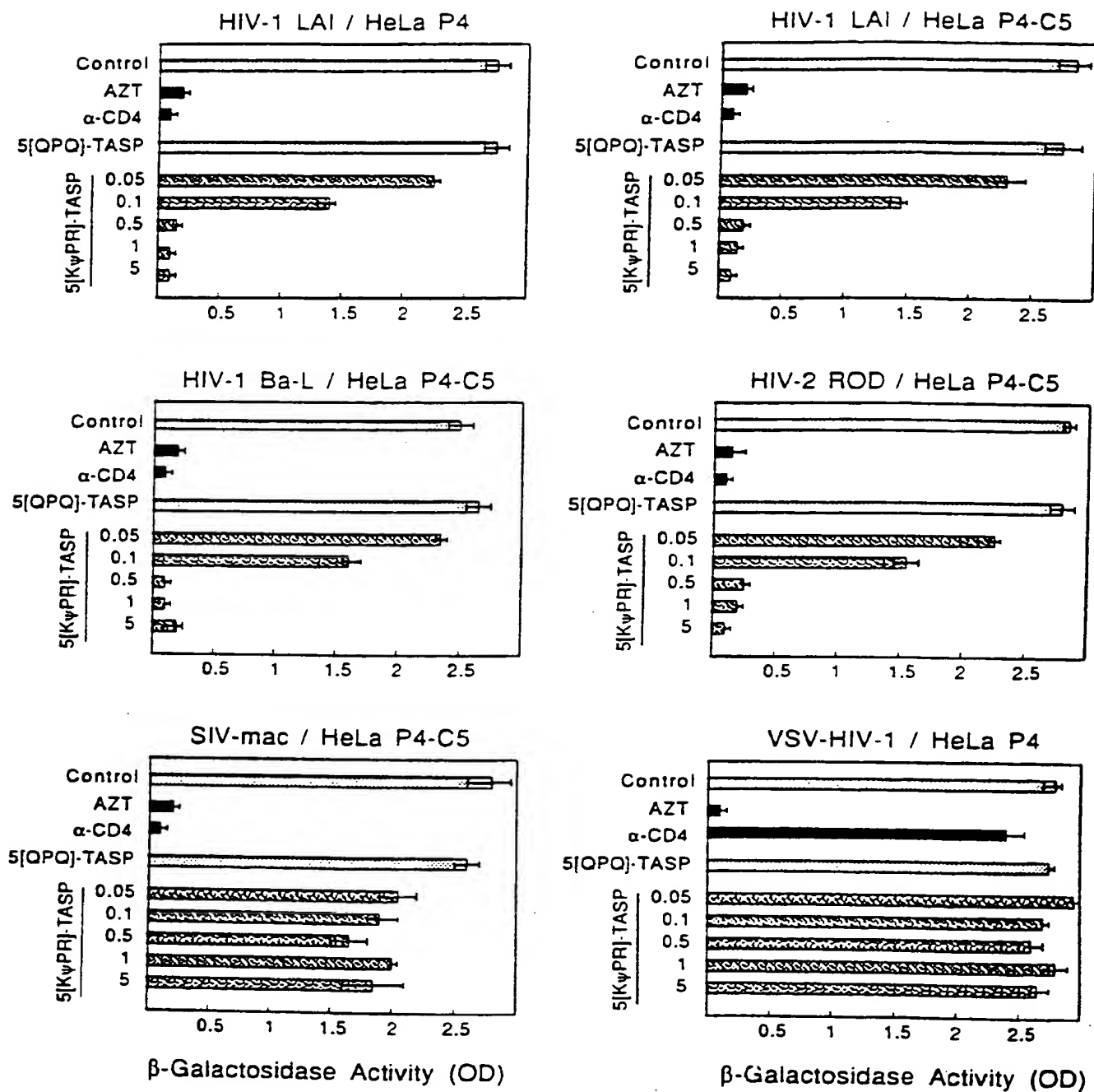


FIGURE 28

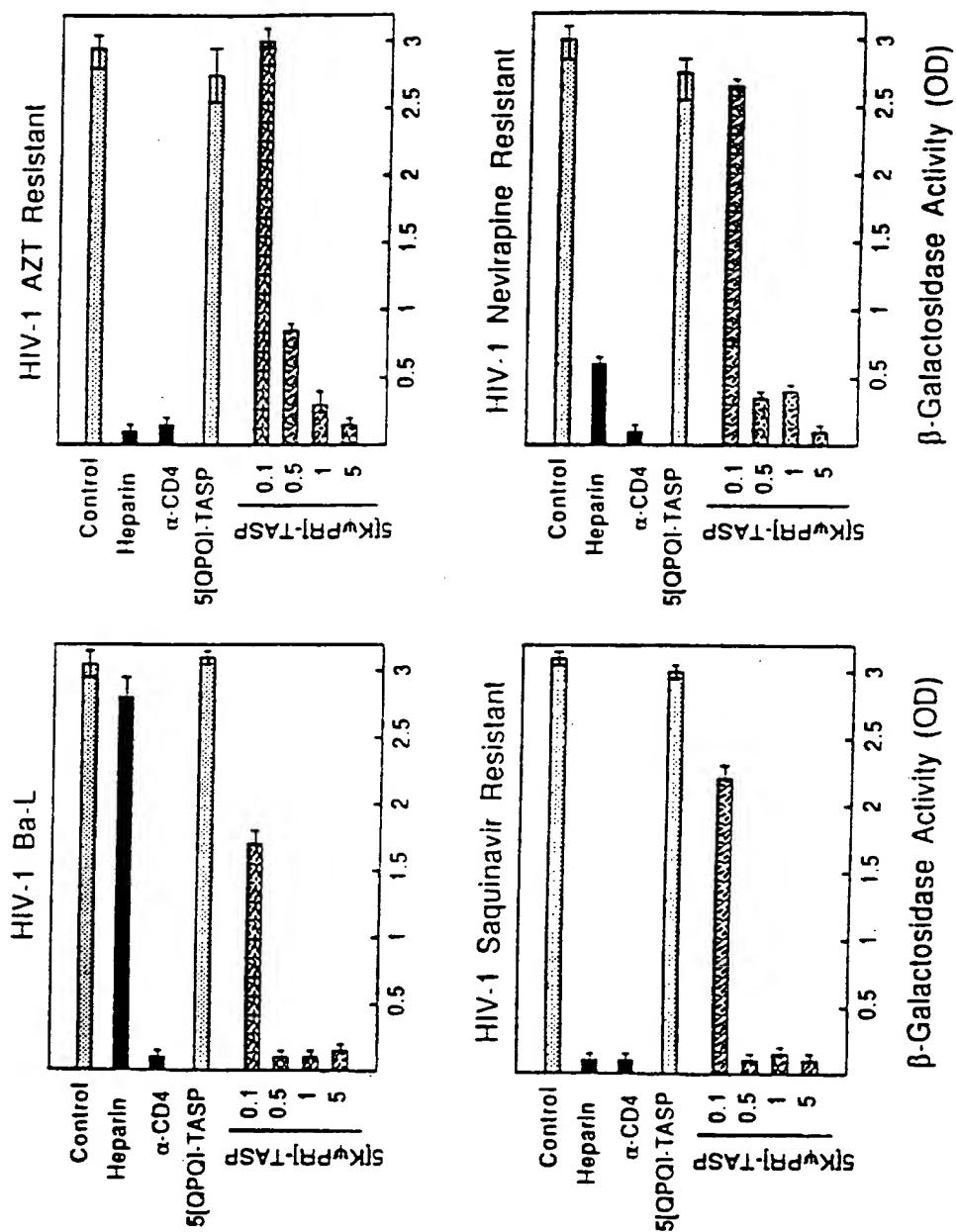


FIGURE 29



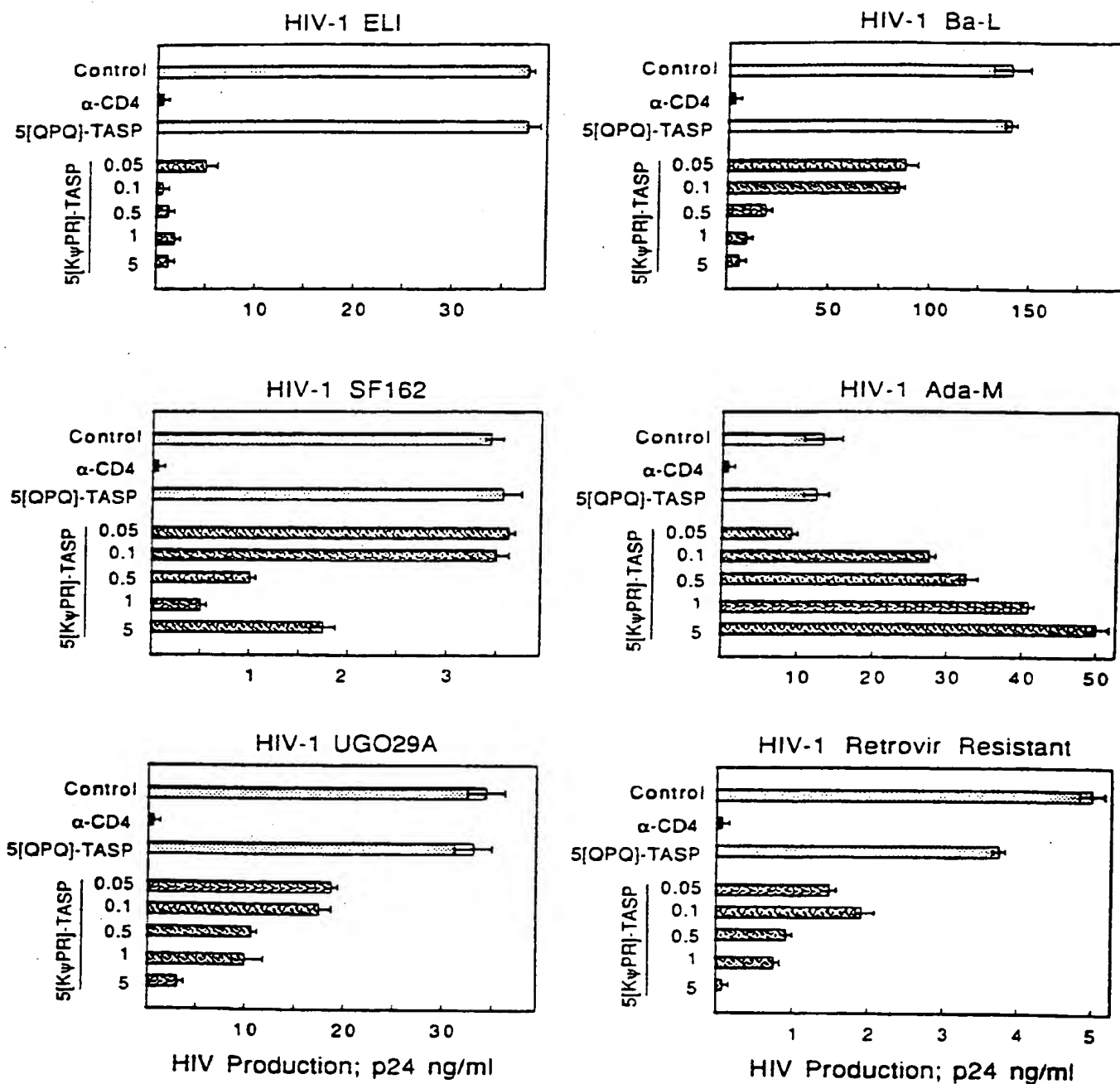


FIGURE 30

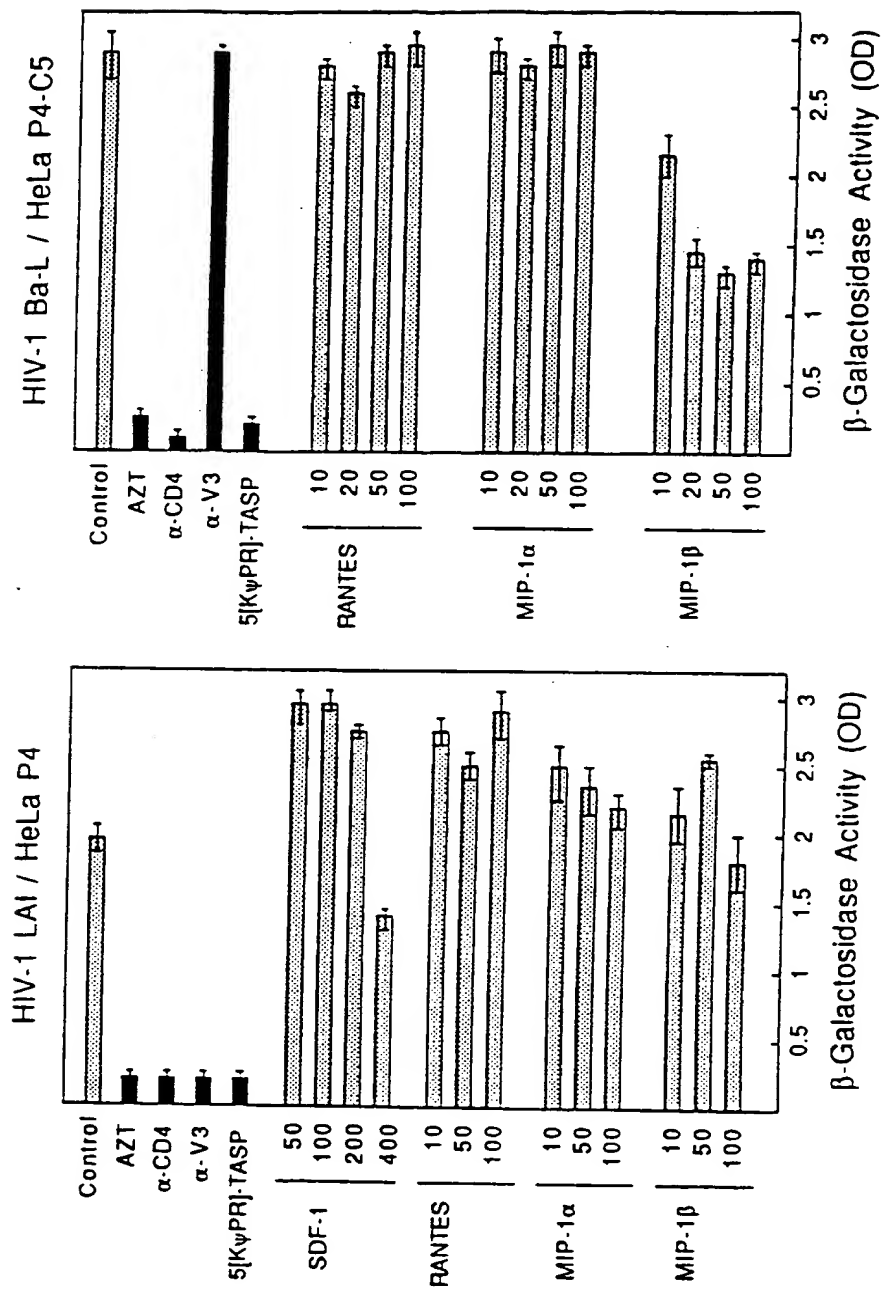


FIGURE 31

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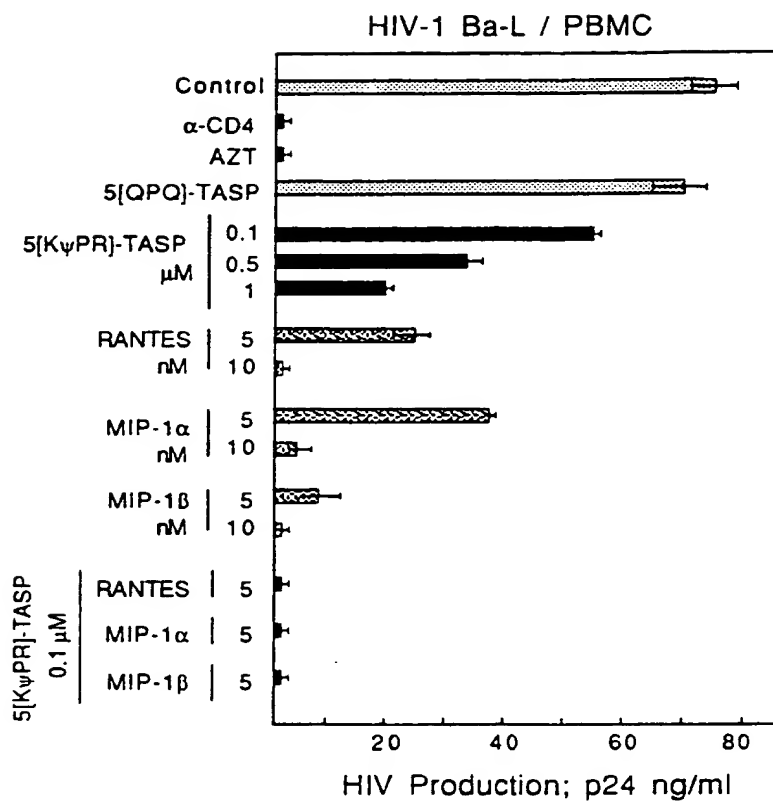


Figure 32

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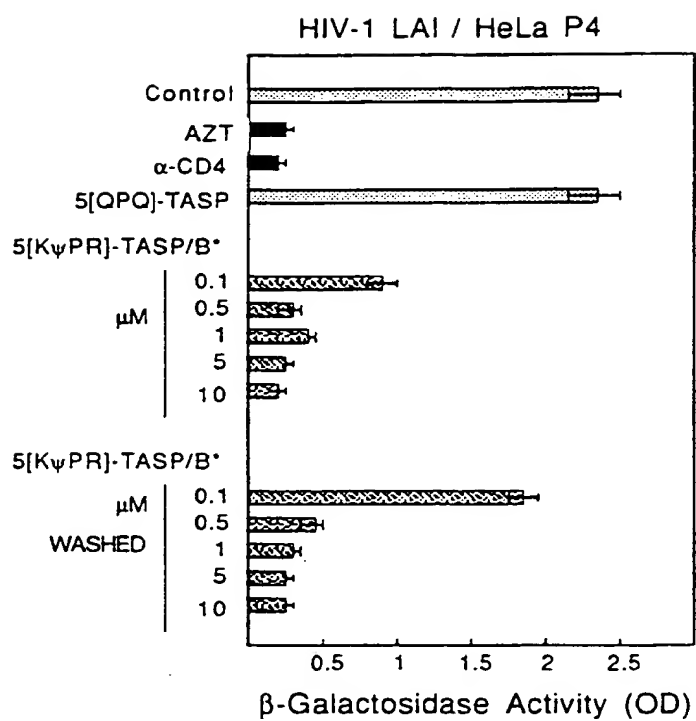


Figure 33

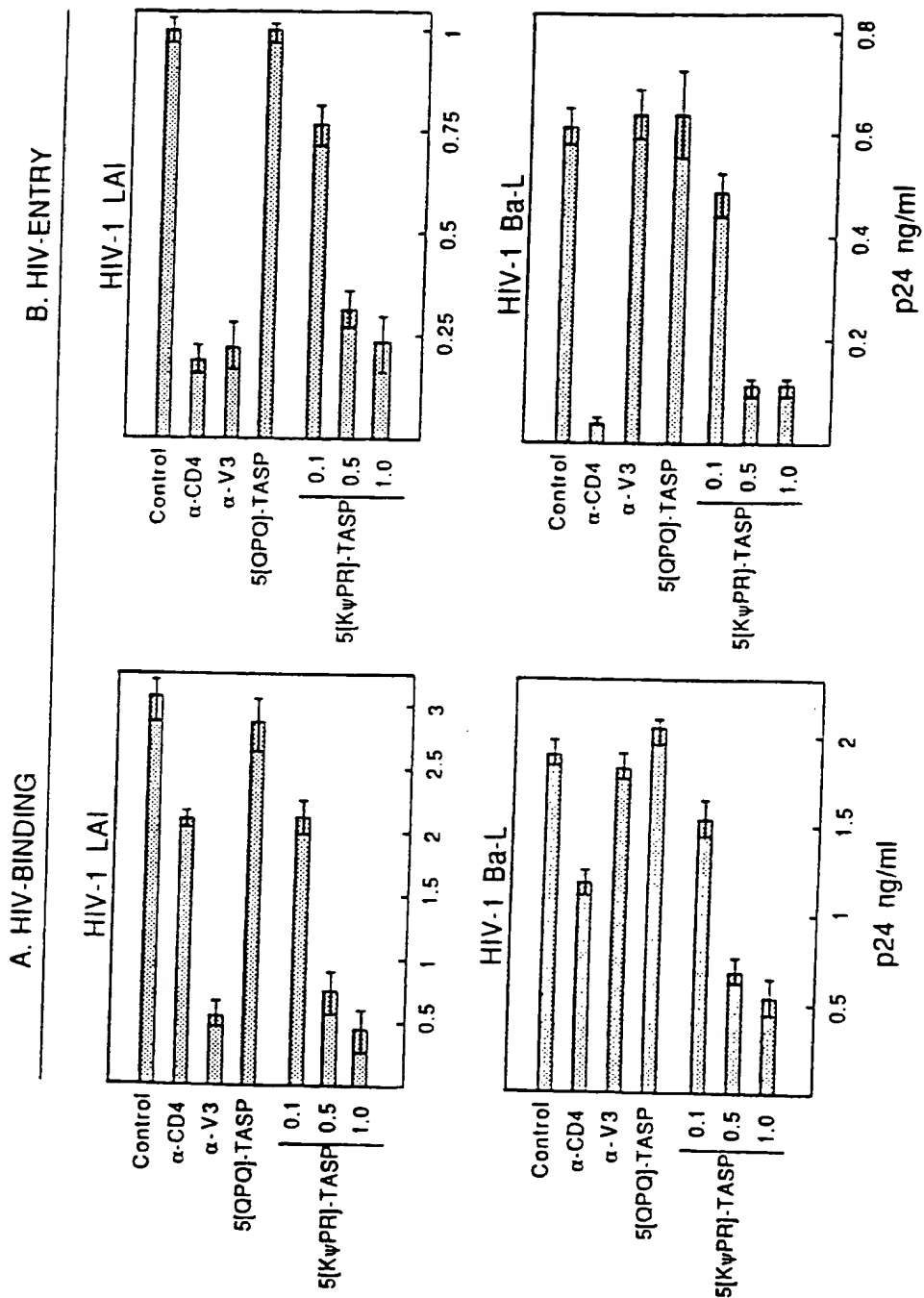


FIGURE 34

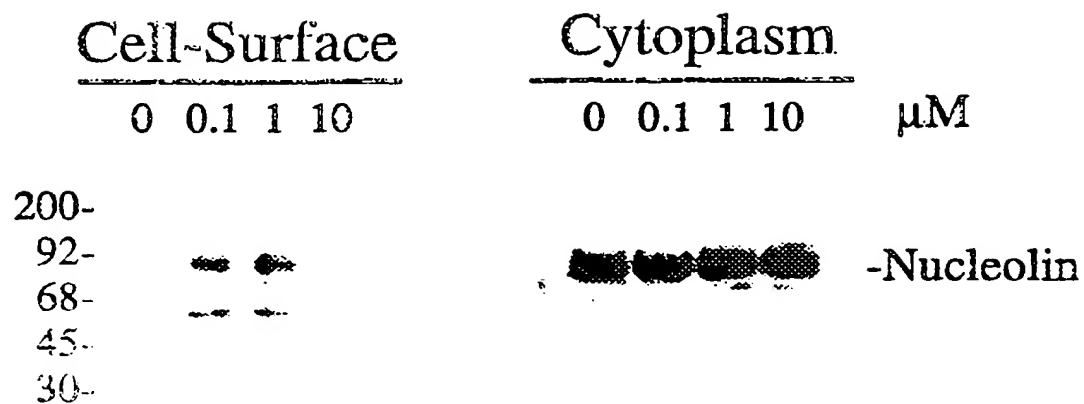


Figure 35

# Cell-Surface

1 2 3 4

≡

-Nucleolin (p95)

1: 1 hr; 2: 1 hr; 3: 6 hr; 4: 24 hr.

2, 3, 4: 5  $\mu$ M

Figure 36

The effect of heparin at  $\mu\text{g/ml}$  on HIV infection in HeLa P4-C5 cells.

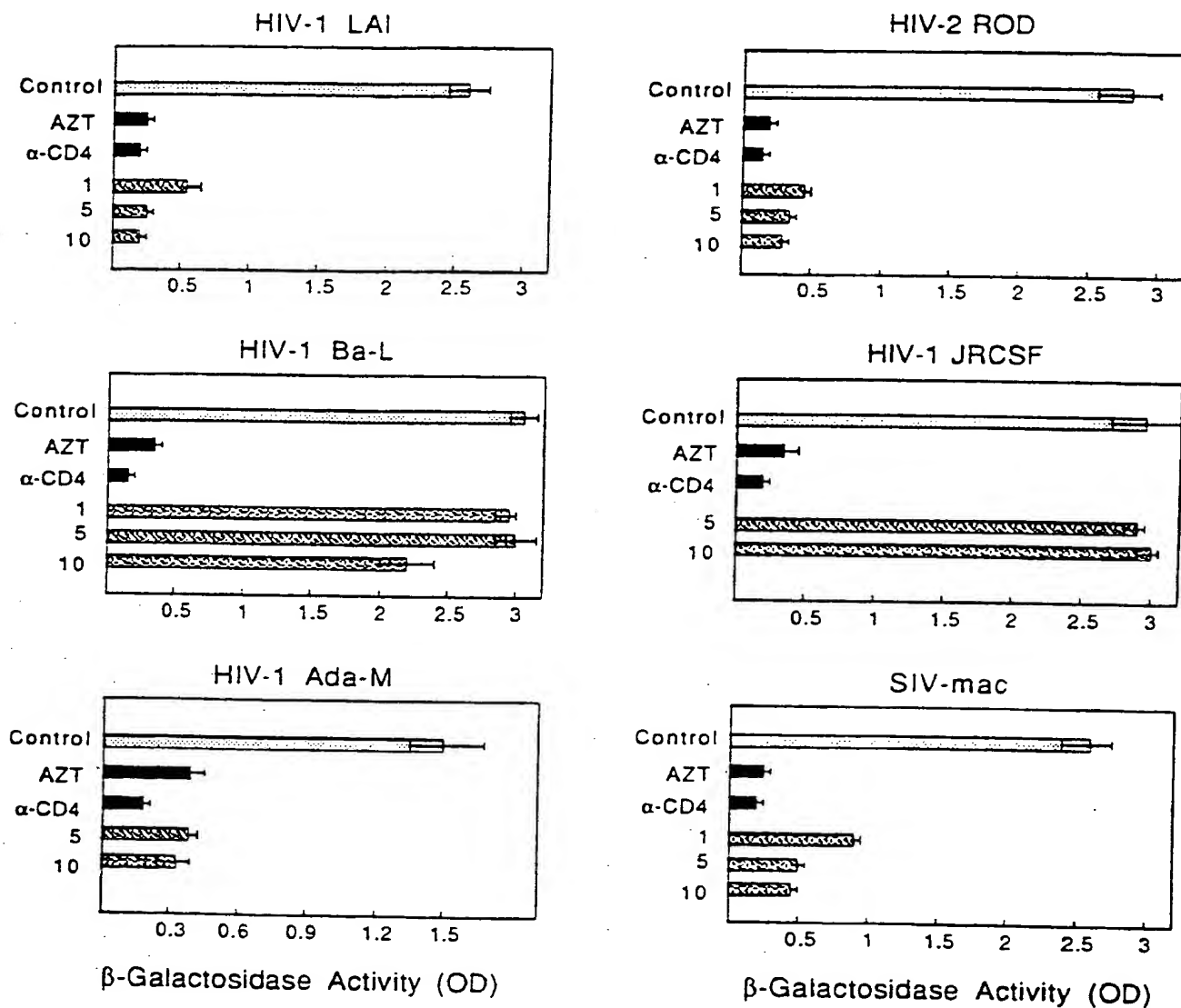
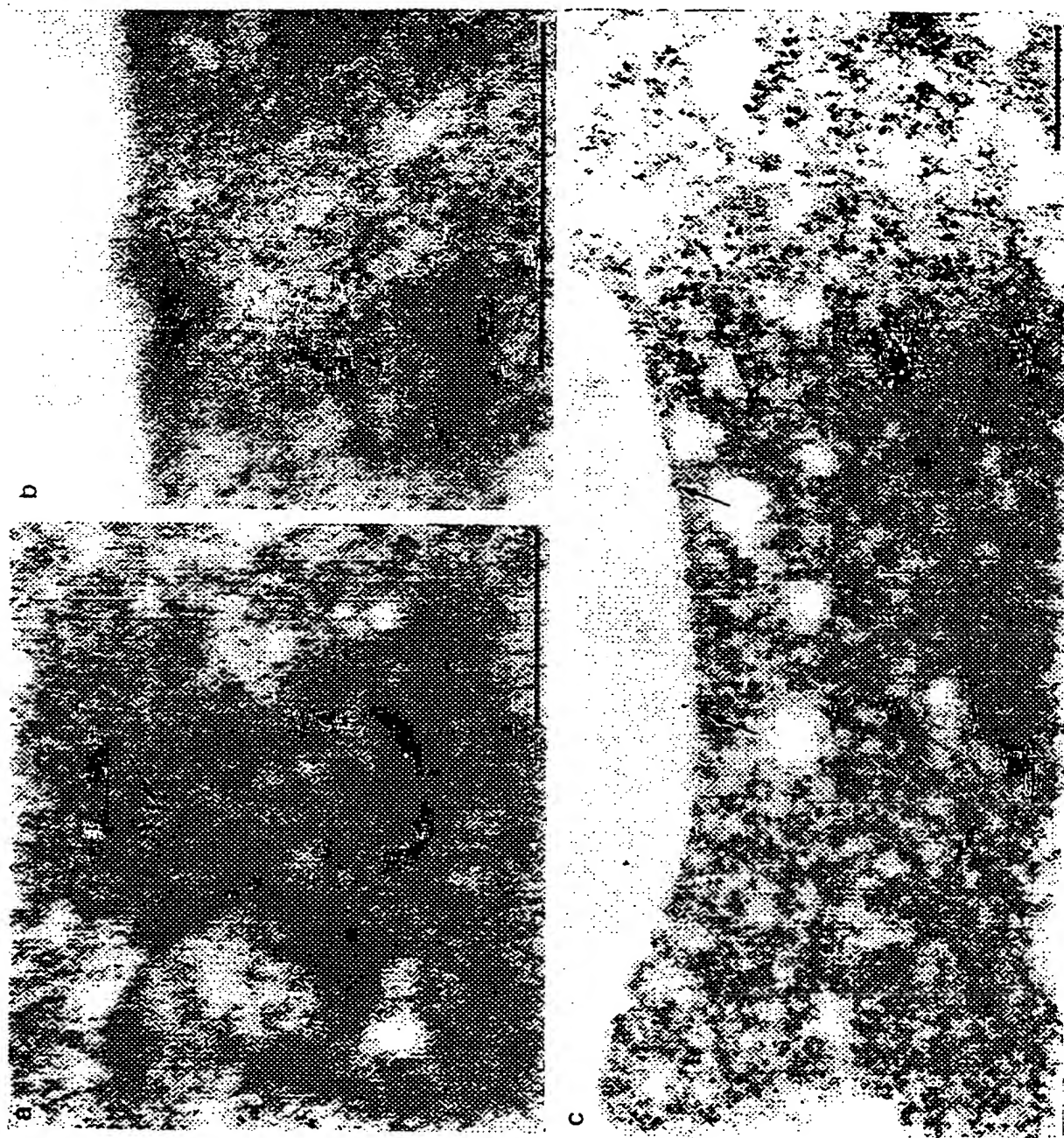


Figure 37





BEST AVAILABLE COPY

FIGURE 33

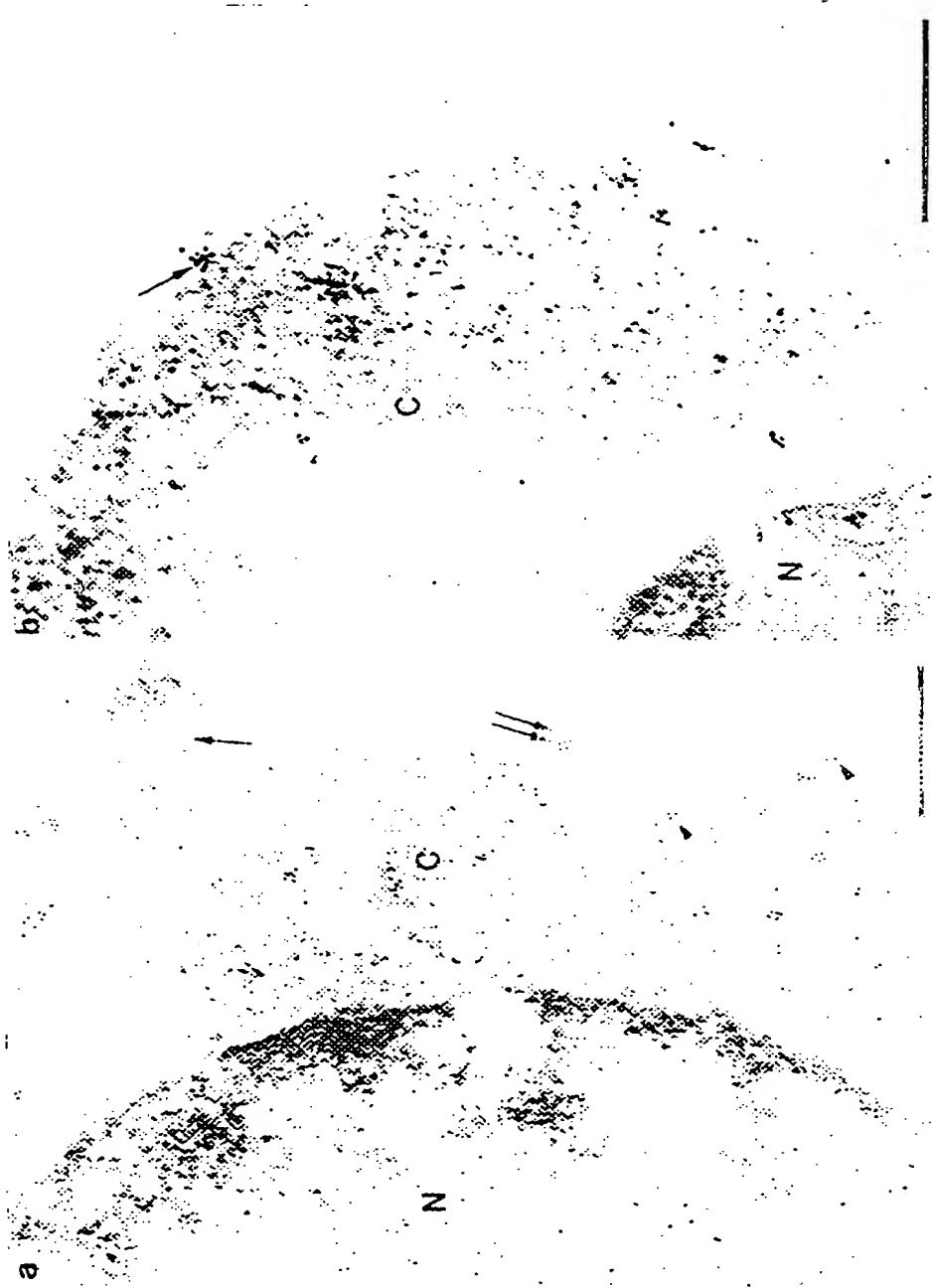


FIGURE 39

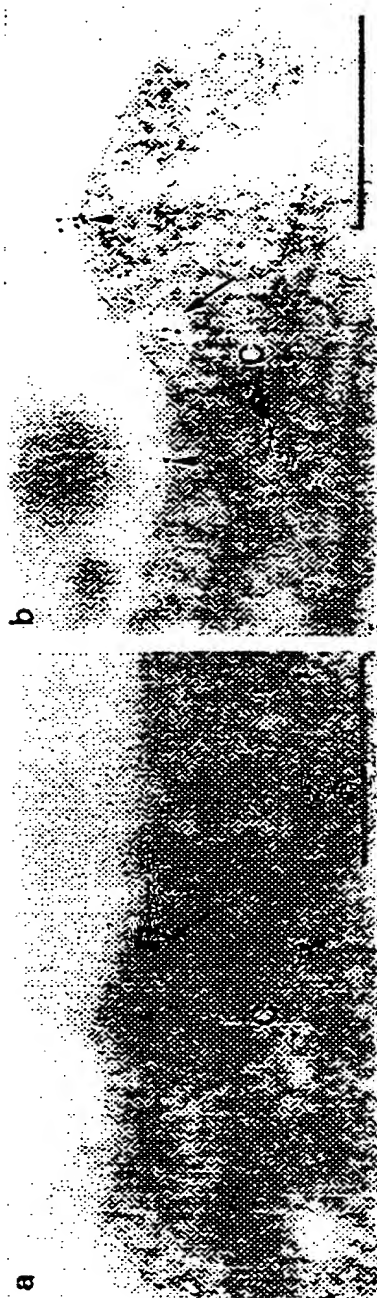


FIGURE 40A



FIGURE 405

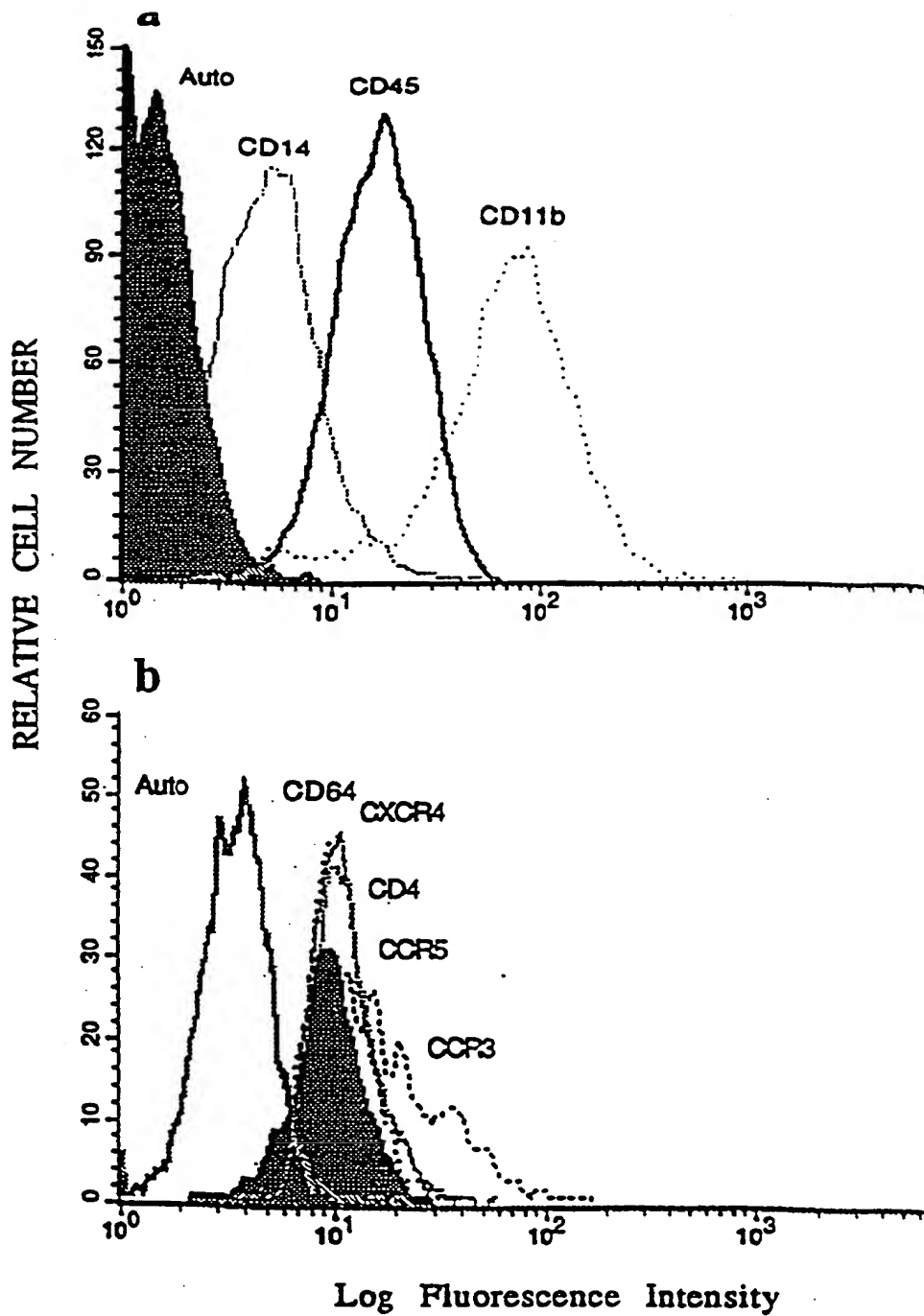


FIGURE 41

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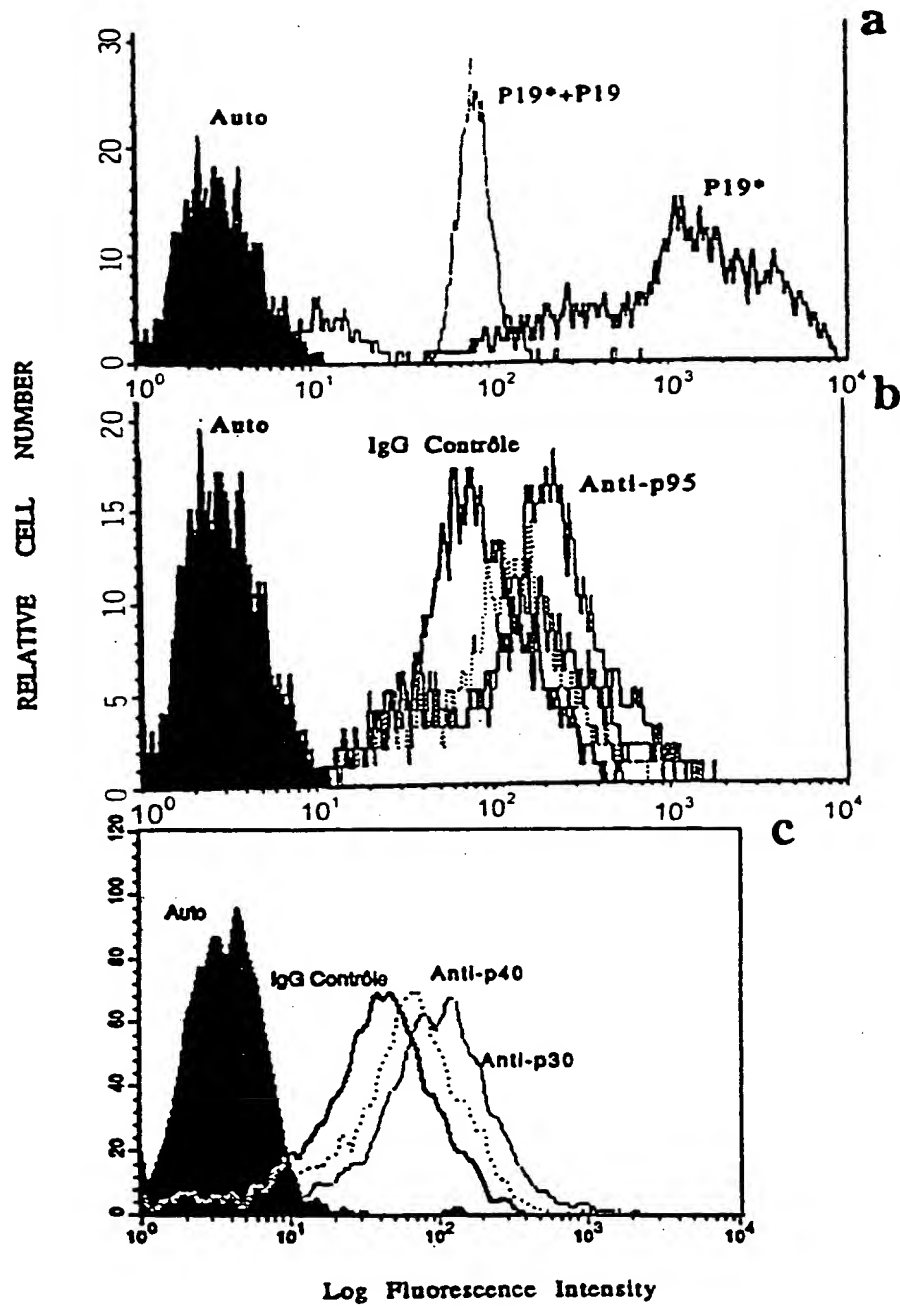


Figure 42

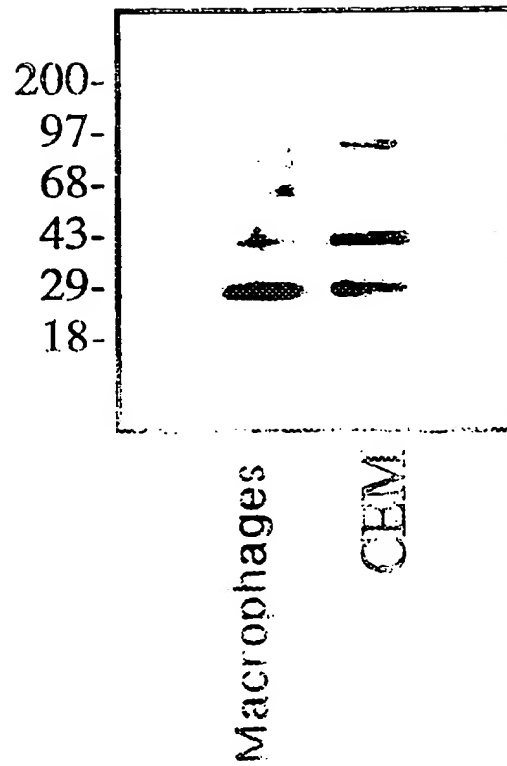


Figure 43

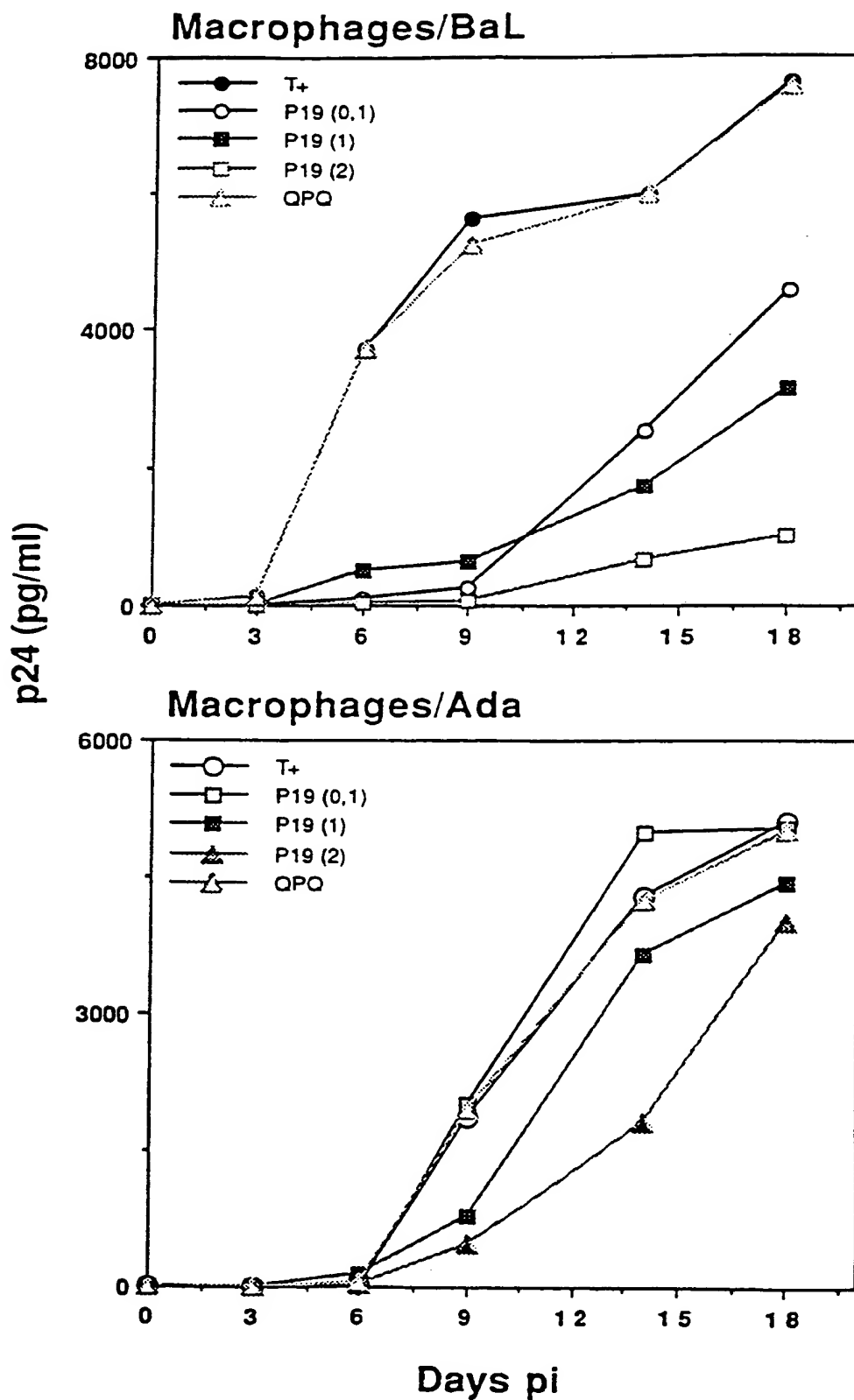


FIGURE 44



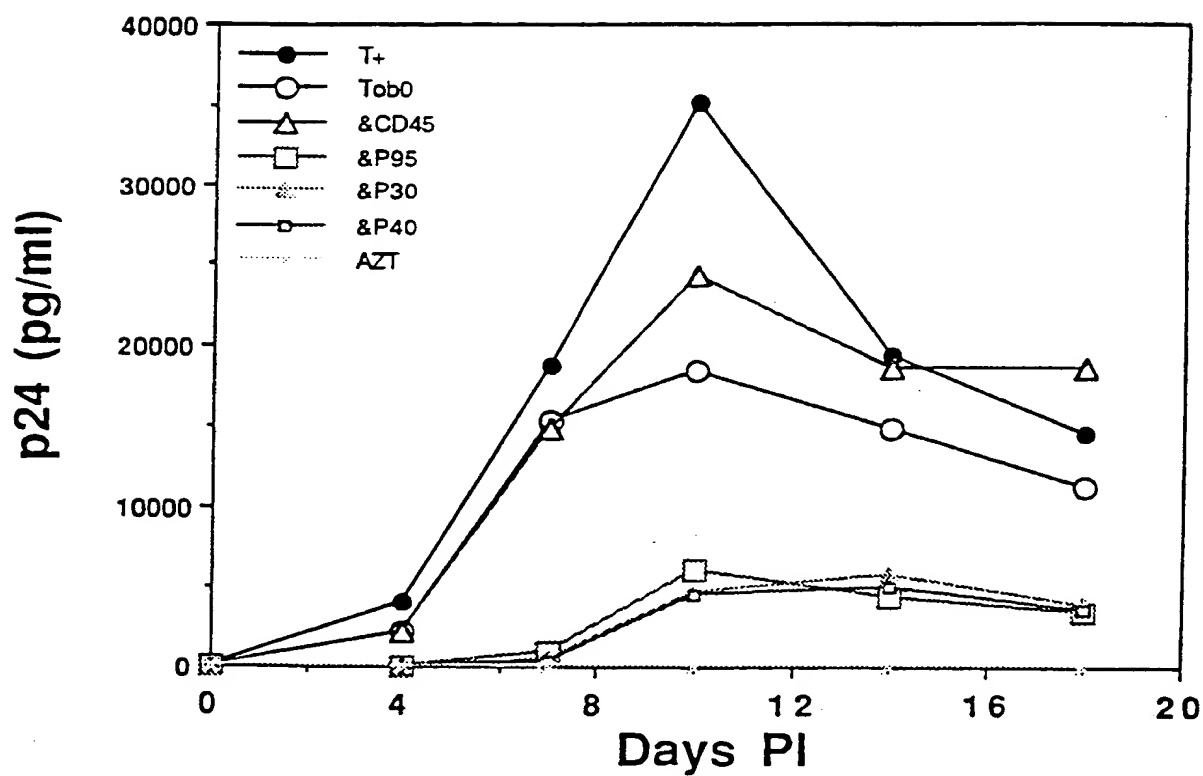


FIGURE 45

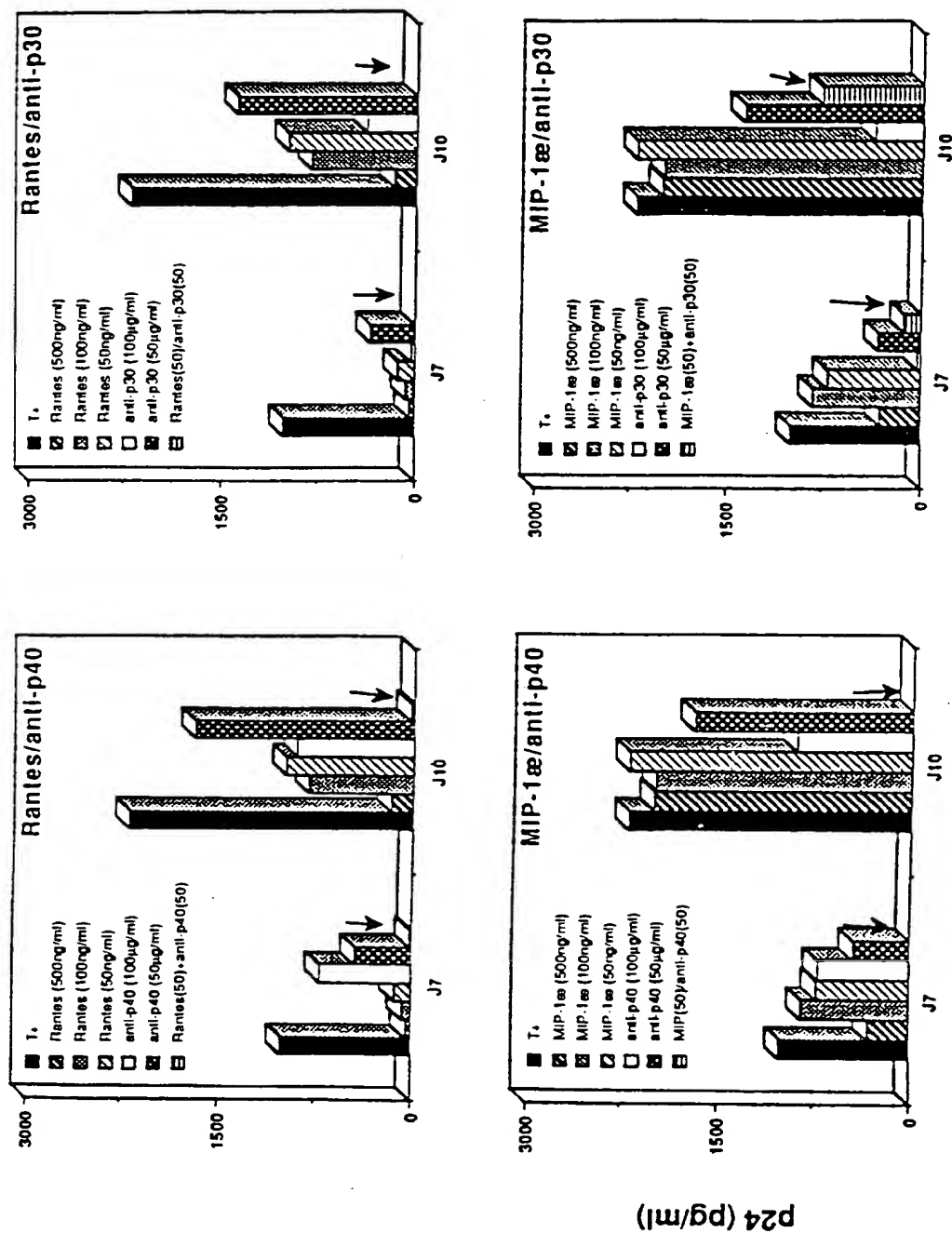


FIGURE 46A

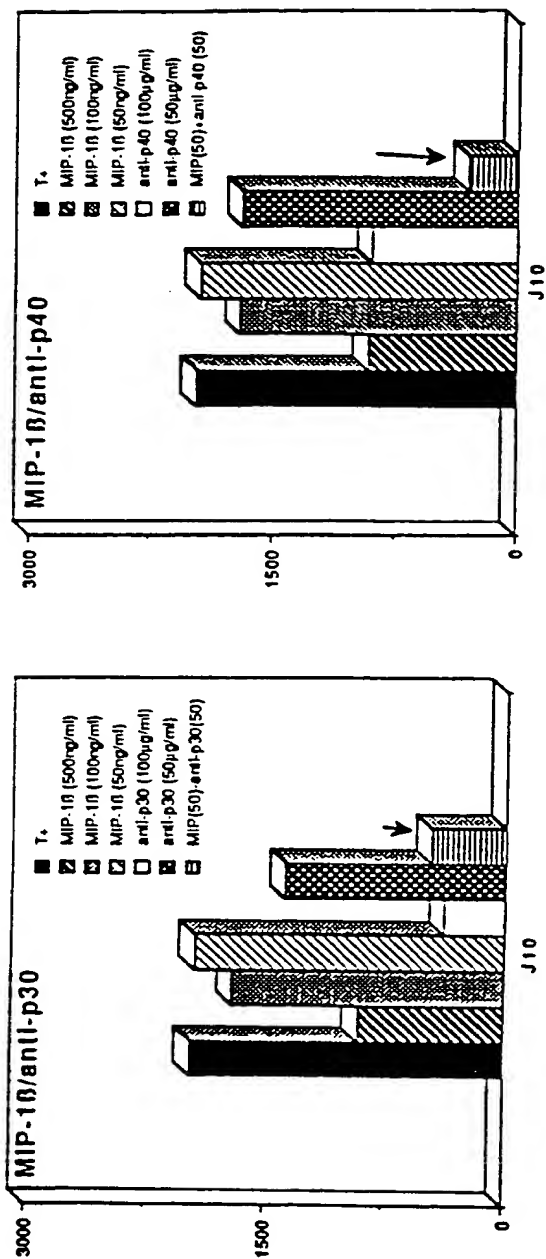


FIGURE 46B

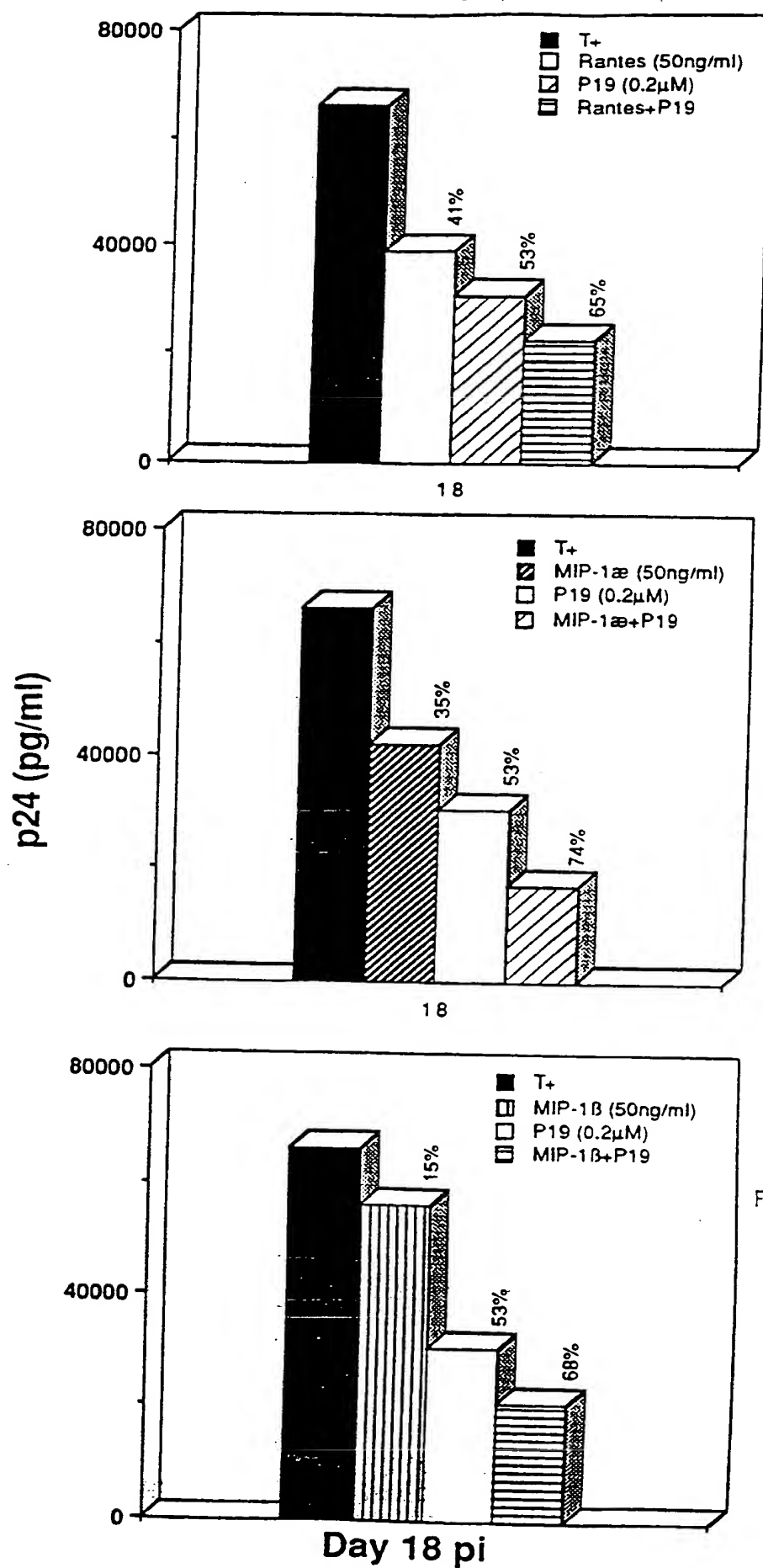


FIGURE 47

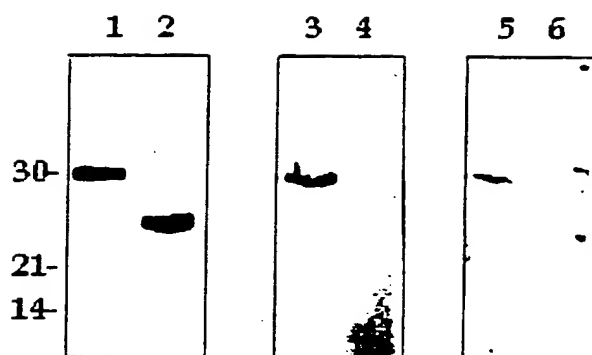


Figure 48

FIGURE 49(1)

I.

/translation="MVKLAKAGKNQGDPPKMAPPPKEVEEDSEDEEMSEDEEDDSSGE  
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AVTTPGKKGATPGKALVATPGKKGAAI PAKGAKNGKNAKKEDSDEEEDDDSEDEEDD  
EDEDEDEDEIEPAAMKAAAAAPASEDEDEDEDEDEDEDDDDDEEDDSEEEAMETTPAKG  
KKA AKVVPV KAKNVAEDEDEEEDDEDEDDDDDEDEDEDDDEEEEEEEEEEPVKEA  
PGKRKKEMAKQKAAPEAKKQKVEGTEPTTAFNLFVGNLNFNKSAPELKTGISDVFKN  
DLAVVDVRIGMTRKFGYVDFESAEDLEKALELTGLKVFGNEIKLEKPKGKDSKKERDA  
RTLLAKNLPYKVTQDELKEVFEDAAEIRLVSKDGKSKGIAYIEFKTEADA EKTFEKQ  
GTEIDGRSISLYYTGEKGQNDYRGGKNSTWSGESKTLVLSNLSYSATEETLQEVFEK  
ATFIKVPQNQNGKSKGYAFIEFASFEDA KEALNSCNKREIEGRAIRLELQGRGSPNA  
RSQPSKTLFVKGLSED TTEETLKE SFDGSVRARIVTDRETGSSKGFGFVDFNSEDAK  
EAMEDGEIDGNKVTLDWAKPKGEGGF GGRGGGRGGFGGRGGGRGGFGGRGRGGFG  
GRGGFRGGRGGGGDH KPOGKKT KFE"

II. 1 ATTCTGCTGT AGACATAGAG ATGATGATCA TAGCTGACTA TGATGATGAT  
51 CCCCCGCGAG CCTGAAAGAG GAAATGCTCT GGT TTGCTAA GCCCGCGAAT  
101 CGAGTGAGAC CCACCCACAA AGCTAACCGT GGAAGTCACT GGCGGCCTCC  
151 TTCGCCCTGC CAGCCGGGGA ACCCATCCGG TGGCTCTCGA CCTGCTCCCG  
201 GGCCATCTGG TGACACTGAC TTCGCAGCCA CCACCTTAAT TGGCGCATTC  
251 GACCCAAATA ATAACCTGGG AACCTGTGGG CGGTCTAAGG CCCGGCTCTG  
301 CGGTCGCCCT CCCAGGCCCC TCTCCCTGGC CCTGTGAGGC CAGAAAGTTA  
351 CTTCTCCGAG GCCAGTTCCC CATGTCTGAG AAATATCTCC CAACTTGAGG  
401 TTCTGTGGGG TAGGGGAGGG TTCGTGACTT TCTCACAGAA AACCTCGTAC  
451 AGACCCCGCC ACTGCCTTTA TTAACAGCTC TCAGGAGACT GCCTGCAGGA  
501 GGGGGGTCGC TCCGGCCCCA TGCTCGCGGG CAAGCAGGGA TAAGCTGTGC  
551 CTCCAAAAGG GCCAACGGGA ACTCCGCGGT CCCTGAACTT CCGGTGCTGG  
601 AGGACTCCTC GCTCCAGGGC CACCAGGAGC CGCGGCGTGA GTGCGTGCCG  
651 GAACCGAGGG CGGGGTCTCT GAGGAACTCC AAGGCTGCCC AAGCCTACGG  
701 ACCCAGCCAC ATTGCGGAAC CGGAGACCGC CCGATTCCAC CACCCCCGCG  
751 CTCCCCTCAC AGCCGGCGCC AAAAACGCCA GTCCCACGAC GCAGGCCGGG  
801 ACCCGCGCGC CCACGGCCCC ATCAGCGCGA CCTTGACAAA AGCGAGCCCC

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FIGURE 49(2)

851 G C C C C C A C G G C G C C G T T G C C A G C C C C T C C C C C T C C C G T G C C G C C T C G G C C  
901 C G C C T A C T C C C G C C C C C G C G C C G T T C A C G G T T A G A G G C T C G C G A T T G G C T  
951 C A T G G G G A C G G C C G C G A G C T T T G G T T G G T C G G C G C G G A G T C A C G A G G C G C  
1001 C G T C G T C G C C T T T C C A C A G G C G T T A C T G G G C A G G C T C A G T C T T T C G C C T C  
1051 A G T C T C G A G C T C T C G C T G G C T T C G G G T G T A C G T G C T C C G G G A T C T T C A G C  
1101 A C C C G C G G C C G C C A T C G C C G T C G C T T G G C T C T T C T G G A C T C A T C T G C G C  
1151 C A C T T G T C C G C T T C A C A C T C G C C G C C A T C A T G G T G A A G C T C G C G A A G G T  
1201 A A A C G G C C T T G A G C G C G A C G C A G A C G T G T A G G C C T G C T T C G A G G G G C G A  
1251 G C G C G G C G C C G C G G G G A G G A G G C C T G C G C G C A G T C C C G G G C G C G T T C T A  
1301 G G G C G C C A T G C T G C G G G A A G T C T C G C G C G A T T A G T G G G G A G G T C T C G C G C  
1351 T T C T G G C T A C T T G G T G G C G A G G T G A A G A G C T T C T G C A G G T G C T G G G G G A G  
1401 G G G G C G C T G G G C C T C G G G G T G G A G A G A T G A G A C C A A A C T T T T G C G A C G C G  
1451 T A C G A G C T G G G A C T G A C T C T G A C G C A C G T G C C C G G G A G C G T G C C T G C C A C  
1501 G T G G G C C G G C G T A G G T C T G G A A T C T C C A G A G G G A C C G G G T G C C T T G G G C C  
1551 G G G A A A T G G C G G T A T C G G C C C T A G T C G G A G T C C C G G C T G C G C T C G G A T G T  
1601 C T C C G C C C C G G C C T G G C A A G C C G A T A C G T G T G G G G C C C G G A A G G T G G C T  
1651 C T G C C G C G T G C C T T T T G C G C T G T G T T T C G G G C A A G A G G T G G T C C T G C C A G  
1701 G T A C C C C C A C G T G G C C G C A C C G C C T C T T T A A G G G G C G G G T A G T G C T G G  
1751 G G A A A G G C A T A A G C T T C A T G A G A A A T A A G T A G T A T T T T T A A G T G C C T T  
1801 A A T G A T C T T C A C C G T T A A T T G A T T C A A A T A A G G G T G G T A G A T A A G T A C  
1851 C G G G A T T T G T A G T A T A A A A C A C G G T T G T G C T T A A C T A A G G T A A C G G G A G  
1901 G A G A A A T C A T T T C C T C A G G T G A C T T T T T A C C T T A G G G C A G G T T T T C T G T  
1951 T G G T A A A G C C T G G G A G G A A A A A T G T G G G C G G T T G A G A A G T A G T C C C T C T T  
2001 G C A T T G C C A T C A G G A G T A G T T T C T A T G T T A G T T G T G G T G T T T G G C A C T A T  
2051 G A G A A A T G A T C T G A G A C G G A G A T G A T G G C G T A T G A A C A C T A A T G G C A A A A

FIGURE 49(3)

2101 TATGAATGGC CTGAAATGTC GAGGTGGAGG TGTAATGATC TATTTGTGTC  
2151 CATTTTAGGC AGGTAAAAAT CAAGGTGACC CCAAGAAAAT GGCTCCTCCT  
2201 CCAAAGGAGG TAGAAGAAGA TAGTGAAGAT GAGGAAATGT CAGAAGATGA  
2251 AGAAGATGAT AGCAGTGGAG AAGAGGTAAT TTTATCCAAC TTAATGCAGA  
2301 ATTATGTAA AACTACAAAA TGGAGAGTTA AGACATGAAA TTGGATATCT  
2351 GTGGCAAAAA TAAGATTTTA TCAGGTATGT CTTATTGTAG TGGTTGAGTG  
2401 TTTCACAAGC TCTTCATTGA CATGTCAAGA TGTCATTGG CTAGTATTTG  
2451 AATGTGAGTG CTAAGACGAG ACTGGGAATT TCTTTTACAT GTTCCTCTGC  
2501 AGGGCTTGGA GTGTGATTG TTGTGTTAAA TCATTACATT TTTCCAGTTT  
2551 CAACATGTTA GCTCACCCCC ACATGTAGAG CTGGGCATTG TATTCAGAGC  
2601 TGAGAATAAC CTTACCAGAT TCCTTTCCTA TCCTCCGAAT TAAAATTAAT  
2651 TGGTCTCCAT TCCATATATA TATAACTGTA TCACTACTGG TTAAGTACTC  
2701 GGGTGTAGAC TGAGGGCTGC CACCTCTCTT TGGTACCATT GACCCTCTTT  
2751 AGCCACCTCC TGGCCTTTTA TTTGCCTCCA CTATAAAGAC AGCTGAGCAC  
2801 TGAATTGTGC TCAGGTTTTT GTTGAGAACC TGAATGAAAG TTTTACTCTC  
2851 CACACATTGC CTTGATAAAA CTACGGGATT TTAATGTAGC TAAATGATGA  
2901 CTTTTATCAA ACTACCATGC AACTCTTTG ATGTGTGATA GTTTTGTAAG  
2951 GAATATTTAT ATTTAGCCTA TTCATTTTTT GTCTCAGGTC CTAAGAATTG  
3001 AGCTTCACTG GGCTTGGTGG ACCGCAACCA CGAGGGCCCC AATGATTAA  
3051 TAAGTTAATG CTTGGAGCCT CCTATGTGTA ACGTTCTGAA TAATTTACAC  
3101 ATAGCAATTC ATGACCTTAA ACATGTAAGG ATGATACTAT TACCATTTTC  
3151 AGATGAGAAA GTTGGGGCTT GGGAAAGTAT GAGGTGTAAG AATTCAGAGG  
3201 GTCTGGTTCA GAGGTATTTT CAGTGTTCAA AAGAGTTCCT TATGTCTGGG  
3251 TATTCACCTT ATTATAGGGG CTCTGACTTA AGACAACATA ACAGAAGCCT



FIGURE 49(4)

3301 GGAGTTTTAA CATGTCATAT GTGTCATGCG TATGTCTTGA ACCAGAGGCA  
3351 TTGCCAGAGT CTAACAACCTC ATTGGGACCA TGGTTATCTT TTTGGGTGTG  
3401 GGGCTGGACT TACTGGTTTG GTTTTCATTT ATCTCAAGGT CGTCATACCT  
3451 CAGAAGAAAG GCAAGAAGGC TGCTGCAACC TCAGCAAAGA AGGTGGTCGT  
3501 TTCCCCAACA AAAAAGGTTG CAGTTGCCAC ACCAGCCAAG AAAGCAGCTG  
3551 TCACTCCAGG CAAAAGGCA GCAGCAACAC CTGCCAAGAA GACAGTTACA  
3601 CCAGCCAAAG CAGTTACCAC ACCTGGCAAG AAGGGAGCCA CACCAGGCAA  
3651 AGCATTGGTA GCAACTCCTG GTAAGAAGGG TGCTGCCATC CCAGCCAAGG  
3701 GGGCAAAGAA TGGCAAGAAT GCCAAGAAGG AAGACAGTGA TGAAGAGGAG  
3751 GATGATGACA GTGAGGAGGA TGAGGAGGAT GACGAGGACG AGGATGAGGA  
3801 TGAAGATGAA ATTGAACCAG CAGCGATGAA AGCAGCAGCT GCTGCCCCCTG  
3851 CCTCAGAGGA TGAGGACGAT GAGGATGACG AAGATGATGA GGATGACGAT  
3901 GACGATGAGG AAGATGGTAA GGAGTTGTCT TGGTAGTTAC TGGGCTTCTG  
3951 ATTACAAGGT ATCTTGAGAT TCTGGGATCA CATATTCCTT CATCGTACAA  
4001 CCTGGAGATG AGATTAGAAT CTTGTGGGAA TTCTCTTGGG TTGTTGTGGT  
4051 GTGCTAGACT TAATTACCCA TGAATGATTT TGTCTCTTG AGAAAATTTT  
4101 AATAGCACAT CTATTAGTGT TTTTATAAT GTAGGATTTT CGTTTCTAAG  
4151 TGATTTTTTT TTTTTTTTAA ATTTTTTTGA GATGGAGCTT TTGCTGTTTC  
4201 CCAGGCGGGA GTGCAATGGC GCGCTATCTC GGCGCACTGC AGCCTCCATC  
4251 TCCTGGGTTC AAGCAGTTCT GCCTCAGCCT CCCGAGTAGC GGGATTACAG  
4301 GTGCCCACCA CCACACCCTA CTAATTTTGT ATTTTAGTAG AGACGACATT  
4351 TCACCATGTT GGCCAGGCTG GCTCTGAACT TTGACCTCAG GTGATCCACC  
4401 CACCTTAGGC TCTCCCAAAG TGCTAGGATT ACAGGTGAGA TATGCTGCGC  
4451 CCGGCCCCAA GTGATCTATT CTTGCCATGA CTGTAACTA AACATGGTGA  
4501 CAGGATTCGA TTTTCTTTAC ATTAGATTTG AAAACCGATG TTGGTTTTGG

## FIGURE 49(5)

4551 GAGATTGCTG CAATTTT TAG GTGACTTCTC TTTCAGACTC TGAAGAAGAA  
4601 GCTATGGAGA CTACACCAGC CAAAGGAAAG AAAGCTGCAA AAGTTGTTCC  
4651 TGTGAAAGCC AAGAACGTGG CTGAGGATGA AGATGAAGAA GAGGATGATG  
4701 AGGACGAGGA TGACGACGAC GACGAAGATG ATGAAGATGA TGATGATGAA  
4751 GATGATGAGG AGGAGGAAGA AGAGGAGGAG GAAGGTACTT AAATTAGATT  
4801 CTGACATACG ACATGAGTTA TGTTTAAAGG AGGCACTTAA GTGTTTGTGG  
4851 CTACTGATGT GTGATACATT GTTTGACATC TTGTCCAGAG CCTGTCAAAG  
4901 AAGCACCTGG AAAACGAAAG AAGGAAATGG CCAAACAGAA AGCAGCTCCT  
4951 GAAGCCAAGA AACAGAAAGT GGAAGGTAAC TTGCAGAATT AGGGGATATG  
5001 GGGGAGATAA ACAGCACAAA TGATGAATAA CAAAGGGACT TAATACTGAA  
5051 ACCAGATGTT ACATTGTAGT GTGCTGATGT GCTGTGTATA GAAATTTTGC  
5101 TTTGGAAACT AACTTTTTTAC CACACTACAA GTAGACTGAG TTGAGCTTTT  
5151 TTTGTGCAGG CACAGAACCG ACTACGGCTT TCAATCTCTT TGTTGGAAAC  
5201 CTAAACTTTA ACAAATCTGC TCCTGAATTA AAAACTGGTA TCAGCGATGT  
5251 TTTTGCTAAA AATGATCTTG CTGTTGTGGA TGTCAGAATT GGTATGACTA  
5301 GGTAGCTGCT TCACTGCACG TTACATACCG TGGGTCTGTT AATTTTTTCT  
5351 TCCCCTGTTA GCACAGTTAC TTTAGCCTGC CACTGTTAAA CATGAATACT  
5401 GTAAACACTT CAAGGTTAGC ATTAGTGAAC TAAGTTAGAA TTAAACTGTA  
5451 GATCCCCTAA GTTGCAATTT CCATAATCAG TCGTAACTTG GTATAGCACA  
5501 GAATAATTTT TAGTAATTTT TTTGTTGTTT TTGTTATGTA TTGAGACGGA  
5551 CGCTGGCTTT TGTTCAGGCT GGAGTACAGT GGCGCAATCT TGGCTCACTG  
5601 CAACCTCTGC CTCCCGGGTT CAAGCGATTC TCCTGCCTAA CCTCCCAAGT  
5651 GACTGGGATA CGGGTGCCAC TCACCATGCA TGGCTAATTT TTGTTTTGTA  
5701 TTTAGTATCG ATTTCACCAT GTTGGTCGGC TGGTTTTGAA CTCCTGACCT

FIGURE 49(6)

5751 CAAGTGATCC ACCCACCTCG GCCTCTCGAA GTGCTGGTAC AGCGTCACCA  
5801 CCCTGCCAGT AAGTTTTAAT AATTTGGTGT TAGGTGGGAG AATGCTTGAA  
5851 CCTGGGAGGC AGAGGTTGCA GTGAGCCAAG TTCGCGCCAC TGTACTCCAG  
5901 CCTGGGCAAC AGATTGAGAC ACCGTCTCAA TTTAAAATAA TGTTTATTTT  
5951 CTTGGAAGTA CCTTGAAACT ATTAGACCTG TCTAGTCATC ATAGTGAATA  
6001 CTTTTATCCA GACAGGATTC TCCTGTATTA GTGCTTATAG GTGTTCTTTT  
6051 GTCAGCTGCT ACTGTGAATT CTTATAAGCA ATTTAGCTCC ATGATGAAGA  
6101 CCTCAAACGT GAATGTGCAT GTCATATCTT CATGCTGAGC CGTGTTCTGT  
6151 AGCTGCAGTT TGCAGAGCCT TGACTTTGTT TTGCTATACT AGGGGTGCTT  
6201 TTTAAATGT GATCTTTGTT TGCACCATCA CATTGTCTA GATACAGATT  
6251 GTGATTTTGA TTTGTGTTTT CACCTGTTGT AATTTTGCCC TCCTCTCCAC  
6301 CTGAAGGAAA TTTGGTTATG TGGATTTTGA ATCTGCTGAA GACCTGGAGA  
6351 AAGCGTTGGA ACTCACTGGT TTGAAAGTCT TTGGCAATGA AATTAAACTA  
6401 GAGAAACCAA AAGGAAAAGA CAGTAAGAAA GGTATGTAAG GCTTTATGAG  
6451 TTATGCAATG AACTCAGGAG CTAGACTGCT AGGGAAAATG CTTTGTAACC  
6501 CATTTCCCTT TGGTTTCCTC TTATTTTTTT TAAATCATTT TTTTCCTTTG  
6551 GTTTCCTCTT AATGTGGGAA TTAAATGAGC TACAGTGTTT ACAAGGTA  
6601 TGGCACTGCT TGTCAGTGTA TAGGTAAATT CCTGAGTTAG GCAAGCAAGA  
6651 GCACTCTTAT ACAGAACAAG AACCATTACA TGCACCTAAA TTAAGCTAAG  
6701 GATCTTTCTT CACTGAACT AGTTAGGTCC CTAATTACTC CCTATATACA  
6751 GTGTAATGTT TTGAATTGGT ACATTCACCT TTTTGTGTTAT GCGCGTCTAC  
6801 TCTAGGTTGA ACTCCAGTGT ACCTAACAGA GAGTTTGACA TCAAGGCTGT  
6851 GACAACATGG AGGGACCACT TGTGTGTTGA CACTGCTATA TCTCCATATT  
6901 TAGCACCGAG CCTTGACAT ATAGGATCTC AAATTATTTG TTGATAGAGC  
6951 TATGTGTGTT TTTCCCCTCT TTTTGTTGTT GCCCCCACC TTTGGTTTTT

FIGURE 49(7)

7001 CAGGCCACAG AGCTCATTTT TGTTTTTTTA ATCTAGAGCG AGATGCGAGA  
7051 ACACTTTTGG CTAAAAATCT CCCTTACAAA GTCACTCAGG ATGAATTGAA  
7101 AGAAGTGTTT GAAGATGCTG CGGAGATCAG ATTAGTCAGC AAGGATGGGA  
7151 AAAGTAAAGG GTATGTTCTT CTATTGAAAT GTAAGGGTTT TATTAACATT  
7201 AATGCACTTC CTGCTTTATA AAAGAAATAT TGGTTTGATT TCCTTAGGCG  
7251 TGTAACCTGG ACAGTTTAAC CTGTAAGTTT GTGCCTCAGT AACCCATCTG  
7301 TACCATGGGG ATAATGTACT CATAGGGTGA TTTTAAAAGA CAAAGCTAAT  
7351 ACTTACAAAG AAGCAAGTTT AATGCCTATC TTACATAAAT ACTTTGTAAG  
7401 TAGTAGCAGT TCTTTCAGTG AGGTGAGGTT ACATGAAAAA ATTCCAAGTA  
7451 TTTGTAAAC TAGTGGGAAG TAAGAGGGAA GCTCGAGTTT TGATTGAAAA  
7501 GTGGACTAAA CAAGGGCATT TTATGTACTC AGATCTGAAG CAAGTTCTGT  
7551 GTTGCTGAGG TAAAAGCATT TGTGTTAATA TGGTTTTTAA AACCATGAGT  
7601 TCTTCTCCCT CCATTGCAGG ATTGCTTATA TTGAATTTAA GACAGAAGCT  
7651 GATGCAGAGA AAACCTTTGA AGAAAAGCAG GGAACAGAGA TCGATGGGCG  
7701 ATCTATTTCC CTGTACTATA CTGGAGAGAA AGGTCAAAAT CAAGACTATA  
7751 GAGGTGGAAA GAATAGCACT TGGAGTGGTA AGAAATTAGG CTTGTTCCAA  
7801 GGTTTTCAGA ATTGGTTGAG GGAACCTTC TAGTCTTTGT ATTTCATAAG  
7851 TTTATAAATA CTTTTTAATC AAAGTTACTC AAATGTAGGT GAAGATCAAG  
7901 GACATGATAC CCCAAGTCAT ACTCTTATTT GGAATAGTAA TTTCCAATCT  
7951 TGAAATGAGA GCTCTAAATC ATTTTGCATT GGAATACAGT AGGCAAATCA  
8001 AGCTTCCTTT GTAGGCATGT TTTATACTTT AAATGACTTG ACCATGTGCG  
8051 TTTTGAACTC AGATGATTCT AGGAAAACAG ACCAGTCATC AGCCTATGTA  
8101 AGAACAACCA GCAGGACATT GCAACACGTA CTAGGTACTT AATATGTTGA  
8151 GTAACAGAAA TGGATTTAGC TTACGTCATG AGTATTTGTA TATAACTCAA

## FIGURE 49(8)

8201 GCACTGAAAT TCTTAGGGAA TAGATATTAC TGTTGTGACC GAAGCTGGGA  
8251 CACTGTTTCA GAGTCTTAGG AATGTGGCTC TCTATTTCTGA GGTGAATCAA  
8301 AAACCTCTGGT TTTAAGCAAC CTCTCCTACA GTGCAACAGA AGAAACTCTT  
8351 CAGGAAGTAT TTGAGAAAGC AACTTTTATC AAAGTACCCC AGAACCAAAA  
8401 TGGCAAATCT AAAGGGTAAG ATAATACCTT TGTATCATCA GTTATAGGCC  
8451 TATATATGTC TTAGAGGTCT AAGGACGTAA GGTCATGTGT CCTGTAGAAA  
8501 AAAGCTAAAT AATTTTAGCC TAGTAAATGA GTGTAAAATA AGTATATTTA  
8551 GGTCCAACCT TGAGAGAAGG GCCTTGGCCA GATCATGTGA CCAGTGGTAT  
8601 AGAGAGCATG TGCCTGGTAA ATTACTCTAA GCATTAAGTG TTCATCCTCA  
8651 GGTATGCATT TATAGAGTTT GCTTCATTCG AAGACGCTAA AGAAGCTTTA  
8701 AATTCCTGTA ATAAAAGGGA AATTGAGGGC AGAGCAATCA GGCTGGAGTT  
8751 GCAAGGACCC AGGGGATCAC CTAATGCCAG AAGCCGTAAG TTCACCTGGT  
8801 TAGGGTGCTG TGGTTGGGGG TAGCACTCTC GGTGCTTTGT TTATTTTTCG  
8851 ACAAATTCTG TGTTTCCTGT TCGCTACTGA GTGAACAATA ACTGGATATC  
8901 GATGACTGAT TACCTGAGAA ATAATTGATG AAATCTCAAG AAAATTCCTC  
8951 TAGATAGTCA AGTTCTGATC CAGCTGTCGT CAACTCAGAG TAGCAAGTTT  
9001 GCCCATGATT TCCTGCCCCA TCCACTGGGC CCCACCTGCT TGGGTTGCTT  
9051 TCCCACCTTC CATAGAAGAC TGGGGCAGGA TATCAACTAT GCAATGGCAA  
9101 TTAAAAAATG TAAACCCAGA ATAGCCTTTA CTTTAATTAA GGACTAGTTG  
9151 GCTTAGTTGC TTTTAACTGC TTTTTCATA TAACAAGTAT CTTGGCTAGT  
9201 AGTCATACTA GGCATTGTGC AAATTCAGTG TACGAACTGT GAATTCACAT  
9251 AAATCGCAAA TTTTTTTTTT CTTCCCAGAG CCATCCAAAA CTCTGTTTGT  
9301 CAAAGGCCTG TCTGAGGATA CCACTGAAGA GACATTAAAG GAGTCATTG  
9351 ACGGCTCCGT TCGGGCAAGG ATAGTTACTG ACCGGGAAAC TGGGTCCTCC  
9401 AAAGGGTAAG GGAAGGAAGC GTGAGTGCTG CTTCCACTTG AAGGGGTTTT

FIGURE 49(9)

9451 TGTTCGTGC AGACCTTGAG TCTAATGTGT CTTCTCATTG AGCTCCTTCT  
9501 GTCTATCAGT GGCAGTTTAT GGATTTCGCAC GAGAAGAAGA GAGAATTCAC  
9551 AGAACTAGCA TTATTTTACC TTCTGTCTTT ACAGAGGTAT ATTTAGCTGT  
9601 ATTGTGAGAC ATTCTGGGGT TCAAGCTGTC ACACCAAGTTA GTTTTCCATA  
9651 GAGAGCTACT CTGCTGCACT GGTATCTTTT TCCCAAATAA ACAAGGCTAC  
9701 TTCTGTGGGA TGGCTCCCCA GCATGTACAG TTAAGTTGGG ACATGTGTAG  
9751 TAGGTGCTTT TTATAATGGG CAATTTTCATT TGGTGTCTTA GGTTTGGTTT  
9801 TGTAGACTTC AACAGTGAGG AGGATGCCAA GGAGGCCATG GAAGACGGTG  
9851 AAATTGATGG AAATAAAGTT ACCTTGGA CTGGGCAAACC TAAGGGTGAA  
9901 GGTGGCTTCG GGGGTCGTGG TGGAGGCAGA GCGGCTTTG GAGGACGAGG  
9951 TGGTGGTAGA GGAGGCCGAG GAGGATTTGG TGGCAGAGGC CGGGGAGGCT  
10001 TTGGAGGTAA GGCACGCAGA GATAATGACA CCACATAGCA TGTGCTCTTC  
10051 AGACCCTGTG CCCTGTCACG GTTCCTAATC ACTGGGGAGG AGGAGCTTTG  
10101 TACCCATTCT TTAAACAGTG TCTTGCCTTC CTCCTGTAGG GCGAGGAGGC  
10151 TTCCGAGGAG GCAGAGGAGG AGGAGGTGAC CACAAGCCAC AAGGAAAGAA  
10201 GACGAAGTTT GAATAGCTTC TGTCCCTCTG CTTTCCCTTT TCCATTTGAA  
10251 AGAAAGGACT CTGGGGTTTT TACTGTTACC TGATCAATGA CAGAGCCTTC  
10301 TGAGGACATT CCAAGACAGT ATACAGTCCT GTGGTCTCCT TGGAAATCCG  
10351 TCTAGTTAAC ATTTCAAGGG CAATACCGTG TTGGTTTTGA CTGGATATTC  
10401 ATATAAACTT TTAAAGAGT TGAGTGATAG AGCTAACCTT TATCTGTAAG  
10451 TTTTGAATTT ATATTGTTTC ATCCCATGTA CAAAACCATT TTTTCCTACA  
10501 AATAGTTTGG GTTTTGTTGT TGTTACTTTT TTTTGTGTTT TTGTTTTTTT  
10551 TTTTTTTGCG TTCGTGGGGT TGTAAGAGAA AAGAAAGCAG AATGTTTTAT  
10601 CATGGTTTTT GCTTCACCGC TTAGGACAA ATTAAAGTC AACTCTGGTG

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## FIGURE 49(10)

10651 CCAGACGTGT TACTTCCTAA AGAGTGTTTC CCCTGGAATC TCACTGGAGA  
10701 GCATGGCAAA GCCAGCTCTG CCACTTGCTT CACCCATCCC AATGGAAATG  
10751 GCTTAGTGCG TGTTTCCAGT ATCCCAGCCC TAACTAACTT GGTTGAAATG  
10801 CTGGTGAGGG GACCTGCTCC TGCAGCCCTG GTGCTGACTT GAAGGCTGCT  
10851 GCAGCTTCTC CTACTTTTAG CAGGTCTCGA GGATTATGTC TGAAGACCAC  
10901 TCTGGAAAGA GGTGAGGAA CAGATTAGTC AGGTTTCCTA GG

FIGURE 49(11)

III.

"MEMGRRIHLELRNRTPSDVKELVLDNSRSNEGKLEGLTDEFEEEL  
EFLSTINVGLTSTIANLPKLNKLELSDNRVSGGLEVLAEKCPNLTHLNLSGNKIKD  
LSTIEPLKKLENLKSLDLFNCEVTNLNDYRENVFKLLPOLTYLDGYDRDDKEAPSDA  
EGYVEGLDDEEEDEDEEEYDEDAQVVEDEDEDEEEEGEEEDVSGEEEEDEEGYNDGE  
VDDEEDEEELGEEERGQKRKREPEDEGEDDD"



FIGURE 49(12)

III.

1 GCTGGTTGAG CCTTCAAAGT CCTAAAACGC GCGGCCGTGG GTTCGGGGTT  
51 TATTGATTGA ATTCCGCCGG CGCGGGAGCC TCTGCAGAGA GAGAGCGCGA  
101 GAGATGGAGA TGGGCAGACG GATTCATTTA GAGCTGCGGA ACAGGACGCC  
151 CTCTGATGTG AAAGAACTTG TCCTGGACAA CAGTCGGTCG AATGAAGGCA  
201 AACTCGAAGG CCTCACAGAT GAATTTGAAG AACTGGAATT CTTAAGTACA  
251 ATCAACGTAG GCCTCACCTC AATCGCAAAC TTACCAAAGT TAAACAAACT  
301 TAAGAAGCTT GAACTAAGCG ATAACAGAGT CTCAGGGGGC CTGGAAGTAT  
351 TGGCAGAAAA GTGTCCGAAC CTCACGCATC TAAATTTAAG TGGCAACAAA  
401 ATTAAAGACC TCAGCACAAT AGAGCCACTG AAAAAGTTAG AAAACCTCAA  
451 GAGCTTAGAC CTTTTCAATT GCGAGGTAAC CAACCTGAAC GACTACCGAG  
501 AAAATGTGTT CAAGCTCCTC CCGCAACTCA CATATCTCGA CGGCTATGAC  
551 CGGGACGACA AGGAGGCCCC TGA CTGAGGGCT ACGTGGAGGG  
601 CCTGGATGAT GAGGAGGAGG ATGAGGATGA GGAGGAGTAT GATGAAGATG  
651 CTCAGGTAGT GGAAGACGAG GAGGACGAGG ATGAGGAGGA GGAAGGTGAA  
701 GAGGAGGACG TGAGTGGAGA GGAGGAGGAG GATGAAGAAG GTTATAACGA  
751 TGGAGAGGTA GATGACGAGG AAGATGAAGA AGAGCTTGGT GAAGAAGAAA  
801 GGGGTCAGAA GCGAAAACGA GAACCTGAAG ATGAGGGAGA AGATGATGAC  
851 TAAGTGGAAT AACCTATTTT GAAAAATTCC TATTGTGATT TGACTGTTTT  
901 TACCCATATC CCCTCT

FIGURE 49(13)

IV.

"MSAPAAKVSKKELNSNHDGADETSEKEQQEAIEHIDEVQNEIDR  
LNEQASEEILKVEQKYNKLRQPPFQKRSELIKIPNFWVTTFVNHPQVSALLGEEDEE  
ALHYLTRVEVTEFEDIKSGYRIDFYFDENPYFENKVLSEFHLNESGDPSSKSTEIKW  
KSGKDLTKRSSQTQNKASRKROHEEPESFFTWFTHSDAGADELGEVIKDDIWPNPLO  
YYLVPMDDDEEGEGEEDDDDDDEEEGLEIDIEEGDEDEGEEDDDDEGEEGEEDGED  
D"

IV.

1 CGACCGCGGA GCAGCACCAT GTCGGCGCCG GCGGCCAAAG TCAGTAAAAA  
51 GGAGCTCAAC TCCAACCACG ACGGGGCCGA CGAGACCTCA GAAAAGAAGC  
101 AGCAAGAAGC GATTGAACAC ATTGATGAAG TACAAAATGA AATAGACAGA  
151 CTTAATGAAC AAGCCAGTGA GGAGATTTTG AAAGTAGAAC AGAAATATAA  
201 CAAACTCCGC CAACCATTTT TTCAGAAGAG GTCAGAATTG ATCGCCAAAA  
251 TCCCAAATTT TTGGGTAACA ACATTGTGCA ACCATCCACA AGTGTCTGCA  
301 CTGCTTGGGG AGGAAGATGA AGAGGCACTG CATTATTTGA CCAGAGTTGA  
351 AGTGACAGAA TTTGAAGATA TTAAATCAGG TTACAGAATA GATTTTTATT  
401 TTGATGAAAA TCCTTACTTT GAAATAAAG TTCTCTCCAA AGAATTTTAT  
451 CTGAATGAGA GTGGTGATCC ATCTTCGAAG TCCACCGAAA TCAAATGGAA  
501 ATCTGGAAAG GATTTGACGA AACGTTTCGAG TCAAACGCAG AATAAGCCA  
551 GCAGGAAGAG GCAGCATGAG GAACCAGAGA GCTTCTTTAC CTGGTTTACT  
601 GACCATTTCTG ATGCAGGTGC TGATGAGTTA GGAGAGGTCA TCAAAGATGA  
651 TATTTGGCCA AACCCATTAC AGTACTACTT GGTTCCTGAT ATGGATGATG  
701 AAGAAGGAGA AGGAGAAGAA GATGATGATG ATGATGAAGA GGAGGAAGGA  
751 TTAGAAGATA TTGACGAAGA AGGGGATGAG GATGAAGGTG AAGAAGATGA  
801 AGATGATGAT GAAGGGGAGG AAGGAGAGGA GGATGAAGGA GAAGATGACT  
851 AAATAGAACA CTGATGGATT CCAACCTTCC TTTTTTTAAA TTTTCTCCAG  
901 TCCCTGGGAG CAAGTTGCAG TCTT

2.

FIGURE 49(14)